

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 03:59:42 ; Search time 61.68 Seconds
(without alignments)
1295.779 Million cell updates/sec

Title: US-09-657-631-10

Perfect score: 2382

Sequence: 1 LHWTKMDFLISLMTFVFM.....GTAIEAIISSLPKPERLMYFI 462

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2345	98.4	456	10	Q9SPM8
2	1740	73.0	468	10	Q9FVC2
3	1710	71.8	466	10	Q9AUI5
4	1684	70.7	462	10	Q9XFC9
5	1681.5	70.6	455	10	Q9FEA6
6	1662.5	69.8	455	10	Q9SPM6
7	1647.5	69.2	447	10	Q9SLV4
8	1528.5	64.2	407	10	Q9AVN8
9	1421.5	59.7	467	10	Q9SPM7
10	1404.5	59.0	463	10	Q9FVC3
11	1365.5	57.3	447	10	Q9FUI1
12	1241	52.1	472	10	Q9SPM5
13	1240.5	52.1	471	10	Q9SQC2
14	1238	52.0	472	10	Q9W7B3
15	1211	50.8	326	10	Q9AUI4
16	540	22.7	556	3	Q9UT35

17	529.5	22.2	461	5	Q76268	Q76268 drosophila
18	529.5	22.2	464	5	Q9V018	Q9V018 drosophila
19	488.5	20.5	428	4	Q96RX0	Q96RX0 homo sapien
20	478.5	20.1	479	5	Q9XU84	Q9XU84 caenorhabd
21	461.5	19.4	556	3	Q9C2M0	Q9C2M0 neospora
22	451.5	19.0	522	3	Q9HEM6	Q9HEM6 kluyveromy
23	449.5	18.9	553	10	Q94AP8	Q94AP8 arabidopsis
24	436	18.3	555	10	Q94E22	Q94E22 arabidopsis
25	431.5	18.1	483	10	Q9X162	Q9X162 arabidopsis
26	415	17.4	123	10	Q9FS20	Q9FS20 pisum sativ
27	409.5	17.2	510	11	Q92106	Q92106 mus musculu
28	393	16.5	516	10	Q80612	Q80612 arabidopsis
29	379	15.9	405	10	Q9M977	Q9M977 arabidopsis
30	379	15.9	572	3	Q9USP2	Q9USP2 schizosacch
31	374	15.7	493	13	Q90X66	Q90X66 gallus gall
32	356	14.9	495	11	Q921R1	Q921R1 mus musculu
33	329	13.8	508	10	Q9X163	Q9X163 arabidopsis
34	323	13.6	83	10	Q9FS19	Q9FS19 pisum sativ
35	322.5	13.5	606	11	Q9ET10	Q9ET10 mus musculu
36	321.5	13.5	550	4	Q9MTN2	Q9MTN2 homo sapien
37	321	13.5	690	5	Q9BHV5	Q9BHV5 leishmania
38	315.5	13.2	604	4	Q9NQZ7	Q9NQZ7 homo sapien
39	236.5	9.9	1052	10	Q49676	Q49676 arabidopsis
40	152.5	6.4	626	5	Q76144	Q76144 neospora ca
41	147.5	6.2	300	11	Q9D813	Q9D813 mus musculu
42	121	5.1	739	16	Q97FD2	Q97FD2 clostridium
43	119.5	5.0	62	10	Q9SLQ3	Q9SLQ3 solanum mel
44	119	5.0	3241	2	Q9AHF9	Q9AHF9 fusobacteri
45	115	4.8	1058	10	Q9LZ05	Q9LZ05 arabidopsis

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	456 AA.
Q9SPM8	Q9SPM8			
AC	Q9SPM8			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	NOD FACTOR BINDING LECTIN-NUCLEOTIDE PHOSPHOHYDROLASE.			
LN	LN.			
OS	Lup. japonicus.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;			
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.			
OX	NCBI_TaxID=34305;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. Gifu; TISSUE=ROOT;			
RX	MEDLINE=99444909; PubMed=10517321;			
RA	Roberts N.J., Brigham J., Wu B., Murphy J.B., Volpin H.,			
RA	Phillips D.A., Etzler M.E.			
RT	A Nod factor-binding lectin is a member of a distinct class of			
RT	aprases that may be unique to the legumes."			
RD	Mol. Gen. Genet. 262:261-267(1999).			
DR	EMBL: AF156707.1; AF006609.1;			
DR	InterPro: IPR000407; GDAI_CD39_NTPase.			
DR	Pfam: PF01150; GDAI_CD39_1.			
DR	PROSITE: PS01238; GDAI_CD39_NTPASE; 1.			
KW	lectin; Hydrolase.			
SQ	SEQUENCE 456 AA: 49933 MW: 62418728EA459DC2 CRC64;			

Query Match	98.4%;	Score 2345;	DB 10;	Length 456;
Best local similarity	100.0%;	Pred. No. 1.3e-170;		
Matches 456;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	7	MDFLISLMTFVFMALPAISSOTLGNIIIMNRKILLPKNOEPTVSTAVIFDAGSTGSRVH 66		
DB	1	MDFLISLMTFVFMALPAISSOTLGNIIIMNRKILLPKNOEPTVSTAVIFDAGSTGSRVH 60		

aprases

see below

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QY 67 VYNFQNDLDPVENELEFYDVKPGIJSYAANPEEAESLIPLKEAENVVPSQOPMT 126
DB 61 VYNFQNDLDPVENELEFYDVKPGIJSYAANPEEAESLIPLKEAENVVPSQOPMT 120
QY 127 PVYLGATAGRLLEGNAEENILOAVDMLSNRSALNVQSDAVSILDGTQEGSYLWNTINY 186
DB 121 PVYLGATAGRLLEGNAEENILOAVDMLSNRSALNVQSDAVSILDGTQEGSYLWNTINY 180
QY 187 LIGKLRKRTKTYGVVDLGGGSVQMTYAVSRNTAKNAPVPGEDEPYIKKVLQCKKVDL 246
DB 181 LIGKLRKRTKTYGVVDLGGGSVQMTYAVSRNTAKNAPVPGEDEPYIKKVLQCKKVDL 240
QY 247 YVHSYLRGRFAEIRFVAGGSANPCLLAFGDGAYTYSAGAEYKVSAPASGSNTNOCRK 306
DB 241 YVHSYLRGRFAEIRFVAGGSANPCLLAFGDGAYTYSAGAEYKVSAPASGSNTNOCRK 300
QY 307 IALKALKVAPCPYONCTFGGIMNGGSGQKNLFTSSFYLLSDVGIFFVKNPAKTRP 366
DB 301 IALKALKVAPCPYONCTFGGIMNGGSGQKNLFTSSFYLLSDVGIFFVKNPAKTRP 360
QY 367 VDLKTAALKACTNLEDAKSKYPDLKERDSVEYVCLDLYVYVTLVDGFGDLPQEVYVA 426
DB 361 VDLKTAALKACTNLEDAKSKYPDLKERDSVEYVCLDLYVYVTLVDGFGDLPQEVYVA 420
QY 427 NEIEYODALVEAAMPGLTAIEAISLPRFERLMTFI 462
DB 421 NEIEYODALVEAAMPGLTAIEAISLPRFERLMTFI 456

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RESULT 2

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Q9FVC2 PRELIMINARY; PRT; 468 AA.
ID 09FVC2:
AC 09FVC2:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE APYRASE GS52.
OS Glycine soja.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3848;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ROOT;
RX MEDLINE=20496172; PubMed=11043467;
RA Day R.B., McAlvin C.B., Loh J.T., Denny R.L., Wood T.C., Young N.D.,
RA Stacey G.;
RT "Differential expression of two soybean apyrases, one of which is an
RT early nodulin.";
RL Mol. Plant Microbe Interact. 13:1053-1070(2000).
DR EMBL: AF207688; MAG32860.1;
DR InterPro: IPR000407; GDAI_CD39_NTPase.
DR Pfam: PF01150; GDAI_CD39_1.
DR PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
SQ SEQUENCE 468 AA; 51817 MW; F9804817D014DB40 CRC64;

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Query Match 73.0%; Score 1740; DB 10; Length 468;
 Best Local Similarity 73.4%; Pred. No. 2e-124;
 Matches 339; Conservative 51; Mismatches 66; Indels 6; Gaps 5;

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QY 4 TKAMDFLISLMTFVFM--PAISSQYLGNNITLNRKILLPKNQEPVSYAVIFAGST 61
DB 10 TKAMDFL-TLFTLLILFTLSTQYHDGNTILTHRKIFPK-QEATISYAVIFAGST 67
QY 62 GSRVHYVNFQNDLDPVENELEFYDVKPGIJSYAANPEEAESLIPLKEAENVVPS 121
DB 68 GSRVHYVNFQNDLDPVENELEFYDVKPGIJSYAANPEEAESLIPLKEAENVVPS 127
QY 122 QQNTPVKIGATAGRLLEGNAEENILOAVDMLSNRSALNVQSDAVSILDGTQEGSYLW 181
DB 128 LYFTTPVKGATAGRLLEGNAEENILOAVDMLSNRSALNVQSDAVSILDGTQEGSYLW 187

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QY 182 VTINILKLGKRTKTYGVVDLGGGSVQMTYAVSRNTAKNAPVPGEDEPYIKKVLQCK 241
DB 188 VTINILKLGKRTKTYGVVDLGGGSVQMTYAVSRNTAKNAPVPGEDEPYIKKVLQCK 247
QY 242 KKYDLYVHSYLRGRFAEIRFVAGGSANPCLLAFGDGAYTYSAGAEYKVSAPASGSNT 301
DB 248 KKYDLYVHSYLRGRFAEIRFVAGGSANPCLLAFGDGAYTYSAGAEYKVSAPASGSNT 307
QY 302 NQCRKIALKALKVAPCPYONCTFGGIMNGGSGQKNLFTSSFYLLSDVGIFFVKNPAKTRP 360
DB 308 DEGREVYVQALKLMESCPHONCTFGGIMNGGSGQKNLFTSSFYLLSDVGIFFVKNPAKTRP 367
QY 361 NAKTRPVDLKTAALKACTNLEDAKSKYPDLKERDSVEYVCLDLYVYVTLVDGFGDLP 420
DB 368 NSKIHVPDLEIEAKRACETKLEDAKSKYPDPAE-DRLPVYCLDIAYQYALYTDGFSIDPW 426
QY 421 QEVTVANEIEYODALVEAAMPGLTAIEAISLPRFERLMTFI 462
DB 427 QEVTVANEIEYODALVEAAMPGLTAIEAISLPRFERLMTFI 468

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RESULT 3

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ID 09A015 PRELIMINARY; PRT; 466 AA.
AC 09A015:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE APYRASE.
GN APY1.
OS Medicago truncatula (Barrel medic).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
OX NCBI_TaxID=3880;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ROOT;
RX MEDLINE=21196099; PubMed=11299390;
RA Wood J.R., Uhm T., Ramu S., Nam Y.W., Kim D.J., Penmetza R.V.,
RA Cook T.C., Denny R.L., Young N.D., Cook D.R., Stacey G.;
RT "Differential regulation of a family of apyrase genes from Medicago
RT truncatula.";
RL Plant Physiol. 125:2104-2119(2001).
DR EMBL: AF288132; AAK15160.1.
DR InterPro: IPR000407; GDAI_CD39_NTPase.
DR Pfam: PF01150; GDAI_CD39_1.
DR PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
SQ SEQUENCE 466 AA; 51561 MW; 122A9004A2D882DF CRC64;

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Query Match 71.8%; Score 1710; DB 10; Length 466;
 Best Local Similarity 69.7%; Pred. No. 3.8e-122;
 Matches 324; Conservative 60; Mismatches 77; Indels 4; Gaps 3;

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QY 1 LHM--TKAMDFLISLMTFVFM--PAISSQYLGNNITLNRKILLPKNQEPVSYAVIFDA 58
DB 3 LHMQTKNMNMNMTLITFLFIMPISYSQYLGNNITLNRKIFPK-QEPTISIAVYFDA 61
QY 59 GSTGRVHYVNFQNDLDPVENELEFYDVKPGIJSYAANPEEAESLIPLKEAENVV 118
DB 62 GSTGRVHYVNFQNDLDPVENELEFYDVKPGIJSYAANPEEAESLIPLKEAENVV 121
QY 119 PVSQOPNTPVKIGATAGRLLEGNAEENILOAVDMLSNRSALNVQSDAVSILDGTQEGS 178
DB 122 PEDQSKTPIRIGATAGRLNGDASEKILQSVHDSNRSSTFNVPQDPAVSIIIDGTQEGC 181
QY 179 YLWTVINILKLGKRTKTYGVVDLGGGSVQMTYAVSRNTAKNAPVPGEDEPYIKKVL 238
DB 182 YLWTVINVALNLGKKFTKTYGVMDVGGGSVQMTYAVSRNTAKNAPVPGEDEPYIKKVL 241
QY 239 LOGKKYDLYVHSYLRGRFAEIRFVAGGSANPCLLAFGDGAYTYSAGAEYKVSAPASG 298

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Query Match	70.7%	Score 1684	DB 10	Length 462
Best Local Similarity	68.5%	Pred. No. 3,6e+120		
Matches 319	Conservative	68	Mismatches 71	Indels 8
				Gaps 5
QY	1 LHM---	TKAMDELISLMTFVFMKPAISSQYIGNNILMNKRIILPKNOEPTSYAVIF	56	
Db	1 MMVMPKTKRSFLL	-LTFELFLSPKLTSSSQYGVNSILNHRKIIP-NQELLTSYAVIF	58	
QY	57 DAGTSGSVHYVNPQNIDLLPVEMLEPYDSVKRGLSSYANPEAASSLPIPLKEAN	116		
Db	59 DAGSGSRVHFVNFQNIIDLHIGNDLEFKTKIKPGLSSYADKPEAAASLLPLLEEAD	118		
QY	117 VVPSQOQNPYVKLGATAGLRLEBNAENIIQAVRDMJNSNSALNVQSDAYSILDTGE	176		
Db	119 VVPELHFKPTPLKLGATAGLRLLDDGAERKIQAVREMRNRSLSIQDAVSVDITGE	178		
QY	177 GSYLMTVNTYLLGKRGKRFKTVGVVDDGGSVQNTYAVSRNTAKNAKPVPEGDEPYIKK	236		
Db	179 GSYLMTVNTYLLGKRGKRFKTVGVVDDGGSVQNTYAVSRNTAKNAKPVPEGDEPYMKK	238		
QY	237 LVLOGKKKVDLYHSYSLARKRGREAFRAEIFKVFAGSASNPCLLACFDGAYTYSGAEGYKSAPA	296		
Db	239 LVLKCKKTDLYHSYSLARKRGNDQAARFKIFPTTGASNPCLLACGEDYIYRKSGESYNIYGT	298		
QY	297 SGSNINQCKRIALKALKLVNAPCPYONCTFFGIGLWNGGSGGOKNLLFTSFYILSDVGIF	356		

ID	Q9FEA6	PRELIMINARY:	PRT:	455 AA.
AC	Q9FEA6			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)			
DE	APYRASE (EC 3.6.1.5) (NUCLEOSIDE TRIPHOSPHATASE) (APYRASE S-TYPE) (S-TYPE APYRAS PRECURSOR).			
GN	NTPIASE.			
OC	Pisum sativum (Garden pea).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spemataophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eucosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.			
OX	NCBI_TaxID=3888;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ALASKA; TISSUE=DARK GROWN STEM INTERNODE;			
RA	Shibata K., Abe S., Davies E.;			
RT	"Structure of the coding region and mRNA variants of the apyrase gene from pea (Pisum sativum).";			
RL	Acta Physiol. Plant. 0:0-0(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ALASKA; TISSUE=DARK GROWN STEM INTERNODE;			
RA	Shibata K., Abe S., Davies E.;			
RT	"Structure of the coding region and mRNA variants of the apyrase gene from pea (Pisum sativum).";			
RL	Acta Physiol. Plant. 0:0-0(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ALASKA; TISSUE=DARK GROWN STEM INTERNODE;			
RA	Shibata K., Morita Y., Abe S., Stanovic B., Davies E.;			
RT	"Apyrase from pea stems: Isolation, purification, characterization and identification of a NTPase from the cytoskeleton fraction of pea stem tissue.";			
RL	Plant Physiol. Biochem. 37:881-888(1999).			
DR	EMBL; AB038668; BAB18895.1; -			
DR	EMBL; AB023621; BAB18890.1; -			
DR	EMBL; AB038554; BAB18893.1; -			
DR	EMBL; AB027613; BAB40230.1; -			
DR	InterPro: IPR000407; GDAL_CD39_NTPase.			
DR	Pfam; PF01150; GDAL_CD39.1.			
DR	PROSITE; PS01238; GDAL_CD39_NTPASE; 1.			
KW	Hydrolase; Transit peptide.			
FT	TRANSIT 1 20 POTENTIAL.			
EQ	SEQUENCE 455 AA; 50106 MW; 5735FE2F5C576111 CRC64;			
QY	Query Match	70.6%;	Score 1681.5;	DB 10; Length 455;
	Best Local Similarity	68.9%;	Pred. No. 5.5e-120;	
	Matches 315; Conservative 64; Mismatches 75; Indels 3; Gaps 2			
DB	1 MEFILKILTFLEFSPAIRTSQYLGNNLLTSRKIFL--KQETISSYAVVFADAGSTGSRH 58			
QY	7 MDELFLSMTFVYMLMPAIISSQYLGNNLLTMKRIILPKQDEPVTSAVYFDAGSTGSRH 66			
DB	1 MEFILKILTFLEFSPAIRTSQYLGNNLLTSRKIFL--KQETISSYAVVFADAGSTGSRH 58			
QY	67 VYNFQNDLLLEVENDELFEYDSVKPPLSSYANPEEAAASLLPLKAEANVVPVSOQPT 126			
DB	59 VYHFNQNDLLHIGKGVETYNKITPELSSYANPEEAAASLLPLLEQAEADVVPDDLOQPT 118			
QY	127 PVKLGATAGLRLLGNAENIIQAAVBDMSNSRSLAVVQSDAVSILDGTGEGSYLWNTVY 186			

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Db 119 PVRIGATAGLRILNGDASEKIIQSVDMLSNRSSTFNVDGDAISIIDGQEGSYLWATYV 178
OY 187 LGKIGKREFTKTVGVYDGGGVOMTYAVSRNTAANAPVPEGDEPYIKLVLGKKYDL 246
Db 179 ALGNLCKRTKTVGVYDGGGVOMAYAVSKRTANAPVADGDDPYIKKVLKCTIPYDL 238
OY 247 VYHSYLRYGREAFAEIEFKVAGSANPCILLAGFDGATYTSAGAEYVSPASGSNLNOCR 306
Db 239 VYHSYLHFGREASRAEILKLTFRSPNCPCLAGFNQIYISGEEFATATYTSGANFNCKN 298
OY 307 IALKALKVNAAPCYONCTFGGIMNGGSGGKNLFTSSFYLLSDVG-IFVKNPNAKIR 365
Db 299 TTRKALKTNPCPYONCTFGGIMNGGSGGKNLFTSSFFYLPRDGTGMVASTPNEFLR 358
OY 366 PVDLTKAAKIACNTLEADKSKYPDLYEKDSVEYVCLDLYVYITLLVDGFLDPQEVTV 425
Db 359 PVDTITKAKKACALNEDAKSTYPLDKKNVASTVCMDLTYOYVLVDGFLDPLQKITTS 418
OY 426 ANEIEYODALVEAMPGLGTAIEAIISSLPKPERLMYFI 462
Db 419 GKEIEYODALVEAMPGLGNVAEIAISLPKPERLMYFI 455

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RESULT 6
O9SPM6 PRELIMINARY; PRT; 455 AA.
AC O9SPM6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE NOD FACTOR BINDING LECTIN-NUCLEOTIDE PHOSPHOHYDROLASE.
GN LNP.
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3879;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ROOT;
RA MEDLINE=99444909; PubMed=10517321;
RA Roberts N.J., Brigham J., Wu B., Murphy J.B., Volpin H.,
RA Phillips D.A., Etzler M.E.;
RT "A Nod factor-binding lectin is a member of a distinct class of
RT apyrases that may be unique to the legumes.";
RL Mol. Genet. 262:261-267(1999).
DR EMBL: AF156782; AAF0611.1;
DR InterPro: IPR000407; GDAI_CD39_NTPase.
DR Pfam: PF01150; GDAI_CD39; 1.
DR PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
KW Lectin; Hydrolase.
SQ SEQUENCE 455 AA; 49879 MW; 68122846D7EC261B CRC64;

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Query Match 69.8%; Score 1662.5; DB 10; Length 455;
Best Local Similarity 68.8%; Pred. No. 1.5e-118;
Matches 315; Conservative 66; Mismatches 72; Indels 5; Gaps 4;
OY 7 MDLFLISM-IFVMLMPAIISSOYLGNLILNKRILLPKNOEPTVSAYVIFDAGSTGSRV 65
Db 1 MEFLTLIAIFLLMLPAITSSOYLGNLILNKRIF--QKEETLTSYAVIFPDAGSGTGRV 58
OY 66 HYNFPOONDLLEVENLEFYDSVKPGLSSYANPEEAESLIPLKEANVPVVSQOPN 125
Db 59 HYNHFOONDLHLTGNDIEFYDKIPGLSAYGNPEQAKSLIPLEEAEDVVPEDLHFK 118
OY 126 TPVKLGATAGLRILNGDAENIIQAVADMLSNSALNVDGDAVSIIDGTOEGSYLWATN 185
Db 119 TPLRLCATAGLRILNGDAEKIIQATRNMFNSRSTLNVDGDAVSIIDGTOEGSYLWATN 178
OY 186 YLIGKIGKREFTKTVGVYDGGGVOMTYAVSRNTAANAPVPEGDEPYIKLVLGKKYD 245

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Db 179 YVLNIGKSFTEKSVGVIDLGGGVOMTYAVSKRTANAPVADGDEPYIKLVLGKKOYD 238
OY 246 LYVHSYLRYGREAFAEIEFKVAGSANPCILLAGDGATYTSAGAEYVSPASGSNLNOCR 305
Db 239 LYVHSYLHFGREARAQVLANATNSANPCILPENGFTTSGYEYKRAFSSSSNFDQCK 298
OY 306 KIALKALKVNAAPCYONCTFGGIMNGGSGGKNLFTSSFYLLSDVG-IFVKNPNAKI 364
Db 299 EILIKVLKVNDCPYPCSTFGGIMNGGSGGOKRLEFYSFAFAYLAEDVGVNEPNSILL 358
OY 365 RPVDLTKAAKIACNTLEADKSKYPDLYEKDSVEYVCLDLYVYITLLVDGFLDPQEVTV 424
Db 359 HPVDFELKARACALNEDAKSTYPLTDKAR-PYVCMDLTYOYVLVHGFGLGRKEIT 417
OY 425 VANEIEYODALVEAMPGLGTAIEAIISSLPKPERLMYFI 462
Db 418 VGEIGIYONSVEAMPGLGTAIVAEIAISLPKPERLMYFI 455

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RESULT 7
O9SLV4 PRELIMINARY; PRT; 447 AA.
AC O9SLV4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE APYRASE (EC 3.6.1.5) (FRAGMENT).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ALASKA; TISSUE=DARK GROWN STEM INTERNODE;
RA Shibata K., Abe S.;
RT "Isolation and identification of a cytoskeleton-associated nucleotide
RT triphosphatase in pea stem cells.";
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB027616; BAA89275.1;
DR InterPro: IPR000407; GDAI_CD39_NTPase.
DR Pfam: PF01150; GDAI_CD39; 1.
DR PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
KW Hydrolyase.
KW NON_TER
SQ SEQUENCE 447 AA; 49065 MW; 7D0F21B2A94BF5D CRC64;

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Query Match 69.2%; Score 1647.5; DB 10; Length 447;
Best Local Similarity 68.8%; Pred. No. 2.1e-117;
Matches 309; Conservative 62; Mismatches 75; Indels 3; Gaps 2;
OY 15 IFVFLMPAIISSOYLGNLILNKRILLPKNOEPTVSAYVIFDAGSTGSRVHYNFPOONL 74
Db 1 TFLFLMPLAITSSOYLGNLILNKRIFL--QKEETLSYAVVFDAGSGSCIHVHFNQNL 58
OY 75 DLLPENLEFEYDSVKPGLSSYANPEEAESLIPLKEANVPVVSQOPTPVKLGATA 134
Db 59 DLHLTGKGVYENKLTTPGLSSYANPEEAESLIPLEQADVDVPPDLOKPTVRLGATA 118
OY 135 GRLLEGAENIIQAVADMLSNSALNVDGDAVSIIDGTOEGSYLWATNLYLIGLKGR 194
Db 119 GRLNGDASEKIIQSVADMLSNRSSTFNVDGDAVSIIDGTOEGSYLWATNLYALGNLKK 178
OY 195 FTKTVGVYDGGGVOMTYAVSRNTAANAPVPEGDEPYIKLVLGKKYDLVYHSYLR 254
Db 179 YTKTVGVYDGGGVOMAYAVSKRTANAPVADGDDPYIKKVLKGIPLYDLVHSHYLF 238
OY 255 GREAPRAEIEFVAGGSANPCILLAGFDGATYTSAGAEYVSPASGSNLNOCRKIALKALKY 314
Db 239 GREASRAEIEILKLTFRSPNCPCLAGFNQIYISGEEFATATYTSGANFNCKNIIKRALKL 298
OY 315 NACPYPONCTFGGIMNGGSGGKNLFTSSFYLLSDVG-IFVKNPNAKIRPVDLKTA 373

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[illegible]

RESULT	8			
09AVN8				
ID	09AVN8	PRELIMINARY;	PRT;	407 AA.
AC	09AVN8;			
DT	01-JUN-2001 (TEMBUREL, 17, Created)			
DT	01-JUN-2001 (TEMBUREL, 17, Last sequence update)			
DT	01-OCT-2001 (TEMBUREL, 18, Last annotation update)			
DE	S-TYPE APYRASE (EC 3.6.1.5) (FRAGMENT).			
OS	Pisum sativum (Garden pea).			
CC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.			
OX	NCBI_TaxID=3888;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ALASKA; TISSUE-DARK GROWN STEM INTERNODE;			
RA	Shibata K., Abe S., Davies E.;			
RT	"Structure of the coding region and mRNA variants of the apyrase gene from pea (<i>Pisum sativum</i>).";			
RL	Acta Physiol. Plant. 0:0-0(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ALASKA; TISSUE-DARK GROWN STEM INTERNODE;			
RA	Shibata K., Morita Y., Abe S., Stankovic B., Davies E.;			
RT	"Ayrase from pea stems: Isolation, purification, characterization and identification of a NTPase from the cytoskeleton fraction of pea stem tissue.";			
RL	Plant Physiol. Biochem. 37:881-888(1999).			
DR	EMBL; AB027615; BAB40231.1; --			
DR	InterPro; IPR000407; GDA1-CD39_NTPase.			
DR	Pfam; PF01150; GDA1-CD39; 1.			
DR	PROSITE; PS01238; GDA1-CD39_NTPASE; 1.			
KW	Hydrolase.			
FT	NOV_TER	1	1	
SEQUENCE	407 AA: 44577 MW: 6403618473059545 CRC64;			

	Query Match	64.28	Score 1528.5	DB 10	Length 407	
	Best Local Similarity	69.88	Pred. No. 2.2e+08			
	Matches	284	Conservative	55	Mismatches	67
					Indels	1
					Gaps	
Oy	57	DAGTSGRVHYVNFDDILLPVENLEEFYDSVRKGLTSYAANDEEAESLIPLKEAEN	116			
Db	1	DAGSTGSRHAYHFHNQNDLLHKGVEGYEYNKRIPGSYSANNDEQAASKSLPLEOARD	60			
Oy	117	VVPSPQCFNTEPVKLGATGADLTLEGNAENTLQAVRMLMSRSALNQSDASTLDCTOE	176			
Db	61	VVPDQLQPTFTVRIGATRTGLFLLNGDASEKLQSVRMLSMRSFTFNWQPDASVTIDBTOE	120			
Oy	177	GSIYMTNTINLYLKLGKGRFKTKGVVDLGGGSVOMTAAVSBNKNAPKVPEGEDPYIKK	238			
Db	121	GSYLMTVITNVNALGNIGKKRYTKTVVIDGSGGSYOMAAVASKTKAKNPVKADGDPPYIKK	180			
Oy	237	LVLGGKKRDYLVHSILYRKREAFPAELFEKVVAGSSANSCLTAGFCAGTAYSGAEEKVAAPA	266			
		: : : : :				
Db	181	VYLKGIPIYDLVHSILHFGREASRAELIKLPBSPNPLLAFNGFIITYTSEEKKAIAIYT	240			
Oy	297	SGSNLNQCRLALKALAKYNACPCFPQNCTPGGITNNGGSGSKNLFLTSSFYLYSEDVG-I	355			
Db	241	SGAANKNKCNTRIALKAIKNYCPQPNCTPGGITNNGGGNGCKNLTFASSSFPLYIPEDIMGV	300			

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OY      356  FVNKNNAIRPDDTAKTLACKNLEBPASKEYDVLXKDSVEVCCDLVYVTLVDGF  415
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB      301  DASTPNEILRPDIETKAKKCALNFBDAKSTYFFLKKNNASVYCHDILQIYLLVDGF  360
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY      416  GIDPQEVTVANEIYQDALVEAMPICGTAIEATSSLPKFERLMYFI  462
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB      361  GIDPQKTTTSGKEIYQDAIVEAMPICGNAAVEATSLPKFERLMYFV  407
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

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RESULT	9	
Q9SPM7		
ID	Q9SPM7	PRELIMINARY; PRT; 467 AA.
AC	Q9SPM7;	
DT	01-MAY-2000	(TREMBLrel. 13, Created)
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001	(TREMBLrel. 13, Last annotation update)
DE	APYRASE.	
OS	Dolichos biflorus (Horse gram).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC	
NCBI_taxonomy	Eucaryotes; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Dolichos.	
NCBI_taxonomy	3840;	
NCBI_taxonomy	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=99444909; PubMed=10517321;	
RA	Roberts N.J., Brigham J., Wu B., Murphy J.B., Volpin H.,	
RA	Phillips D.A., Etzler M.E.;	
RT	"A Nod factor-binding lectin is a member of a distinct class of	
RT	apyrases that may be unique to the legumes.";	
RL	Mol. Gen. Genet. 262:261-267(1999).	
DR	EMBL; AF156781; AAF00610.1; -	
DR	InterPro; IPR000407; GDAI_CDS9_NTPase.	
DR	Pfam; PF01150; GDAI_CDS9; 1.	
DR	PROSITE; PS01238; GDAI_CDS9_NTPASE; 1.	
SO	SEQUENCE 467 AA; 51164 MW; 8FCC200AA60D7376 CRC64;	

Query Match	59.7%	Score 1421.5	DB 10	Length 467
Best Local Similarity	59.6%	Pred. No. 3.9e-100		
Matches 279	Conservative 69	MissMatches 107	Indels 13	Gaps 5
QY	6	ANDFLISLMTPEFMILM----	PAISSQYQGNIIIMNRKILLPKNOEPV-----	TSAAVIF 56
	:		:	:
DB	2	SMDFLILFSLILMTLWLVATATATASSFSLHGKGFKHRKSSSDNNISLEETINESTAVIF 61		
QY	57	DAGSGSRVHYVNFQONLDLPEVNEILFEFYDSKPPKSSSYAANPEEASILPLLEKEAN 116		
	:		:	:
DB	62	DAGSGSRVHYVNFQONLDLRIQGHDLFEVYTKRGLSAYAEENPEEASLPLLEEAA 121		
QY	117	VVPVSOQPTPVKLATAGLRLLLEGNAENIIQAAVADMLSNRSALNVSDAYSILDGTOE 176		
	:		:	:
DB	122	VIPQELHPRTPVKVGATAGLRQLEGDASNRILIQAVSDMLKRSSTLKEGDVAVSNGOE 181		
QY	177	GSLVWTVINYLGLGKRTKTVGVYVDLGGGVQMTYAVSRKPAKNAKPVPEGDEPTLYK 236		
	:		:	:
DB	182	GAYQWTVINYLGNLGNKHKNSKTVAVVDLGGGVQMAVATISEDDAKAPQVPPGVSESYTE 241		
QY	237	LVLGKKKVDLYVHSLTRGRFAFRFIEFVAGSGSNPCLAFEDGAYVTSAGSEVVSAPA 296		
	:		:	:
DB	242	MLLRKKKLYLVHSLTRGGLLAARVVLKSRDSENPCLLSGFDGYTGGVQVYATATAP 301		
QY	297	SGSNLNOCKRIKLKALKVAPCPYONCTFGGIMNGGGGSGQNLFLTSSFYLSDEBVGIF 356		
	:		:	:
DB	302	SGSSFSKCONVLEALHVAHMTSICYDCPTFGGIMNGGGGAGENNPFVASFEEVADAG-F 360		
QY	357	V--NKPNAKIRPVDLKTAALKLACKTNLEDAKSKYPDLYEKDSVEVYCDLVVYVLLVDG 414		
	:		:	:
DB	361	VDPNANALIVRVEDEDAKAVACSTELKDLKSVFPRVKGCD--VPYICLDLVLYQYTLVDG 419		
QY	415	FGLDPFOEYTVANETEXODALVEAMPPLCTALIAETSSLPKPERLWYFI 462		
	:		:	:
DB	420	FGLDPFOEYTVANETEXODALVEAMPPLCTALIAETSSLPKPERLWYFI 467		

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RESULT 10
ID 09FVC3 PRELIMINARY: PRT: 463 AA.
AC 09FVC3:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE APYRASE G550 (FRAGMENT).
OS Glycine soja.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3848;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496172; PubMed=11043467;
RA Day R.B., McAlvin C.B., Loh J.T., Denny R.L., Wood T.C., Young N.D.,
RA Stacey G.;
RT "Differential expression of two soybean apyrases, one of which is an
RT early nodulin."
RL Mol. Plant Microbe Interact. 13:1053-1070(2000).
DR EMBL: AF207687; AGS2959.1; -.
DR InterPro: IPR000407; GDAI_CD39_NTPase.
DR Pfam: PF01150; GDAI_CD39_1.
DR PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
DR NON_TER 463 463
FT SEQUENCE 463 AA; 50435 MW; FCB5B5B8730F7669 CRC64;
SO

Query Match 59.0%; Score 1404.5; DB 10; Length 463;
Best Local Similarity 60.6%; Pred. No. 7,7e-99;
Matches 282; Conservative 62; Mismatches 106; Indels 15; Gaps 7;

QY 8 DELILMTFVFMIPAISSSQ-----YLGNILNRRKILPKNOEPT---SYAVIPDAG 59
DB 4 DYLLILSLSTVLAASSSSSSSSSYLVLGK--FSHRLKLSPIYIIHHTIDESTYAVITDAG 61
QY 60 STGSRVHYVNDQDLPLPENELFEYDSVPGILSTYAANDEEAESLPLKEAENVVP 119
DB 62 STGSRVHYVNRNODDLIRIGODELEFKTMPGISAYAEPNODAESLPLLEEAENVVP 121
QY 120 VSOQNTPVKIGATAGRLLEGNAENILQAVRDMLSNRSALNVQSDAVALDGTGGSY 179
DB 122 QEFHPRTPVKIGATAGRLLEGNAENILQAVRDMLSNRSALNVQSDAVALDGTGGSY 181
QY 180 LMTVINILGKLRKFTKYGVVDLGGGSVQMTYAVSRNTAKNAKPVVEGEDPYIKLTVL 239
DB 182 QMTVINILGKLRKFTKYGVVDLGGGSVQMTYAVSRNTAKNAKPVVEGEDPYIKLTVL 241
QY 240 QGKRYDYVSHSYLRGEARELEFVKYAGGSANPCILAGDGAITYSGAEYKVSAPASGS 299
DB 242 QGKRYDYVSHSYLRGEARELEFVKYAGGSANPCILAGDGAITYSGAEYKVSAPASGS 300
QY 300 NLNOCRKIALKALKVNAFCPYQNTCFGGIWNCGGSGOKNLFITSSPFYSEVVGIFV-- 357
DB 301 SFSQCGVNVVEALHVNATCGYKDCFTFGIWNCGGSGAGENNFFIASFFFEYVADAG--FVDP 359
QY 358 NKRNAKRPVDLTAAKLACTNLEDAKSKYPDLYEKDSVEYVCLDLYVYVTLVDGFGI 417
DB 360 NAENAKRPVDFENAKVACNTLKLKLSFFPRKDG--VPYICLDLYVEYVTLVDGFGI 418
QY 418 DPFQEVYVANEIEYODALVEAAMPILGTATATATATATATATATATATATATATATAT 462
DB 419 DPFQEVYVANEIEYODALVEAAMPILGTATATATATATATATATATATATATATATAT 463

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DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE APYRASE 2.
GN APY2.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3886;
RN [1]
RP SEQUENCE FROM N.A.
RA Jin L., Roux S.J.;
RT "Cloning of a second Apyrase in Pisum sativum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF305783; AAG22044.1; -.
DR InterPro: IPR000407; GDAI_CD39_NTPase.
DR Pfam: PF01150; GDAI_CD39_1.
DR PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
SO SEQUENCE 447 AA; 48783 MW; 5CB2B0CC7A7F660E CRC64;

Query Match 57.3%; Score 1365.5; DB 10; Length 447;
Best Local Similarity 59.0%; Pred. No. 6,9e-96;
Matches 261; Conservative 83; Mismatches 93; Indels 5; Gaps 4;

QY 13 LMTFVFMIPAISSSOYLGNILNRRKILPKNOEPTSYAVIPDAGSGSRVHYVNDQ 72
DB 8 DYLLILSLSTVLAASSSSSSSYLVLGK--FSHRLKLSPIYIIHHTIDESTYAVITDAG 61
QY 73 NDDLPEVNELEFYDSVKGELSSYAANPEEAESLPLKEAENVVPVSOQNTPVKIGTA 132
DB 66 NDDLPEVNELEFYDSVKGELSSYAANPEEAESLPLKEAENVVPVSOQNTPVKIGTA 125
QY 133 TAGRLLEGNAENILQAVRDMLSNRSALNVQSDAVALDGTGGSYLMVTINYLKIG 192
DB 126 TAGRLLEGNAENILQAVRDMLSNRSALNVQSDAVALDGTGGSYLMVTINYLKIG 185
QY 193 KRFETGVGVVDLGGGSVQMTYAVSRNTAKNAKPVVEGEDPYIKLTVLQKRYDYVSHYL 252
DB 186 KRFETGVGVVDLGGGSVQMTYAVSRNTAKNAKPVVEGEDPYIKLTVLQKRYDYVSHYL 245
QY 253 RYGRFAREIFRKYVAGGSANPCILAGDGAITYSGAEYVNSAPASGSNLNOCRKIALKAL 312
DB 246 RYGRFAREIFRKYVAGGSANPCILAGDGAITYSGAEYVNSAPASGSNLNOCRKIALKAL 305
QY 313 KYN-APCPYQNTCFGGIWNCGGSGOKNLFITSSPFYSEVVGIFV--PNAKIRPVDPK 370
DB 306 KYN-APCPYQNTCFGGIWNCGGSGOKNLFITSSPFYSEVVGIFV--PNAKIRPVDPK 365
QY 371 TAAKLACTNLEDAKSKYPDLYEKDSVEYVCLDLYVYVTLVDGFGIDPFQEVYVANEIE 430
DB 366 TAAKLACTNLEDAKSKYPDLYEKDSVEYVCLDLYVYVTLVDGFGIDPFQEVYVANEIE 424
QY 431 YODALVEAAMPILGTATATATATATATATATATATATATATATATATATATATATAT 452
DB 425 YODALVEAAMPILGTATATATATATATATATATATATATATATATATATATATATAT 446

RESULT 12
ID 09SPM5 PRELIMINARY: PRT: 472 AA.
AC 09SPM5:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE APYRASE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
FT STRAIN=CV. NOSSEN (NO-0);

```

RX MEDLINE-99444909; PubMed-10517321;
 RA Roberts N.J., Brigham J., Wu B., Murphy J.B., Volpin H.,
 RA Phillips D.A., Etzler M.E.;
 RT "A Mod factor-binding lectin is a member of a distinct class of
 RT apyrases that may be unique to the legumes.";
 RL Mol. Gen. Genet. 262:261-267(1999).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE-98403884; PubMed-9734815;
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned pl and TAC clones.";
 RL DNA Res. 5:203-216(1998).
 DR EMBL, AF156783; AAF00612.1; -;
 DR EMBL, AB012246; BAB09486.1; -;
 DR InterPro: IPR000407; GDAL_CD39_NTPase.
 DR Pfam: PF01150; GDAL_CD39; 1.
 DR PROSITE: PS01238; GDAL_CD39_NTPase; 1.
 SQ SEQUENCE 472 AA; 51599 MW; FA0C280456D51224 CRC64;

Query Match 52.1%; Score 1241; DB 10; Length 472;
 Best Local Similarity 55.2%; Pred. No. 2.4e-86;
 Matches 245; Conservative 81; Mismatches 112; Indels 6; Gaps 5;

QY 11 ISLMFVFMALPAISSOYLGNILMNRKILLPKNOEPTSTAIVFDAGSTGSRVHYNF 70
 DB 31 IYLGIVLLMLPGRSISDSVEEYSVHNRRKGGPNSRGP-KNYAVIFDAGSGSRVHYCF 89
 QY 71 DONLDLIPVENELEFVDSYKPGLSYAANPEAEESLIPLKEAVNVVVSQOPNTPVKL 130
 DB 90 DONLDLIPVENELEFVDSYKPGLSYAANPEAEESLIPLKEAVNVVVSQOPNTPVKL 149
 QY 131 GATAGTGLRLEGAENIIQAVRDMLSNRSALNVQSDAVSILDGTORGXYLMTINLLGK 190
 DB 150 GATAGTGLRLEGAENIIQAVRDMLSNRSALNVQSDAVSILDGTORGXYLMTINLLGK 209
 QY 191 LCKRFTKTVGVVDLGGGSVQMTYAVSRNTAKNAPVPEGEDPYIKKLVLOGKKYDLVHS 250
 DB 210 LCKRFTKTVGVVDLGGGSVQMTYAVSRNTAKNAPVPEGEDPYIKKLVLOGKKYDLVHS 269
 QY 251 YLRSGEARERAFEFVAGSAPNCILAGDGAITYTSGAATKASAPASGSLNOCRIATK 310
 DB 270 YLRSGEARERAFEFVAGSAPNCILAGDGAITYTSGAATKASAPASGSLNOCRIATK 329
 QY 311 ALKVN-APCPYONCTFGGIMNGGGSGQKNLFLTSSFYLSSEVGIFFV--KPNAKIRPV 367
 DB 330 ALKVN-APCPYONCTFGGIMNGGGSGQKNLFLTSSFYLSSEVGIFFV--KPNAKIRPV 388
 QY 368 DLKTAALACKTNLEDAKSKYIPDLKESVEVCLDLYVYLLVDGFGLDPPQEVTVAN 427
 DB 389 DLKTAALACKTNLEDAKSKYIPDLKESVEVCLDLYVYLLVDGFGLDPPQEVTVAN 447
 QY 428 EIEYODALVEAAMPPLGTAIEAISS 451
 DB 448 EIEYODALVEAAMPPLGTAIEAISS 471

RESULT 13
 ID 09SGG2 PRELIMINARY; PRT: 471 AA.
 AC 09SGG2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE APYRASE.
 GN ATAPY1 OR T6K12.30.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID-3702;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Jeter C.R., Thomas C.E., Roux S.J.;
 RT "Cloning and sequencing of cDNA homologous to pea apyrase.";
 RT submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
 RA Romling C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome III BAC T6K12 genomic sequence.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF093604; AAF00071.1; -;
 DR EMBL, AC016829; AAF26805.1; -;
 DR InterPro: IPR000407; GDAL_CD39_NTPase.
 DR Pfam: PF01150; GDAL_CD39; 1.
 DR PROSITE: PS01238; GDAL_CD39_NTPase; 1.
 SQ SEQUENCE 471 AA; 51193 MW; 6EP17A73207ECDA2 CRC64;

Query Match 52.1%; Score 1240.5; DB 10; Length 471;
 Best Local Similarity 55.1%; Pred. No. 2.6e-86;
 Matches 247; Conservative 74; Mismatches 112; Indels 15; Gaps 6;

QY 11 ISLMFVFMALPAISSOYLGNILMNRKILLPKNOEPTSTAIVFDAGSTGSRVHYNF 66
 DB 31 IYLGIVLLMLPGRSISDSVEEYSVHNRRKGGPNSRGP-KNYAVIFDAGSGSRVHYCF 84
 QY 67 YVNFQDNLDLIPVENELEFVDSYKPGLSYAANPEAEESLIPLKEAVNVVVSQOPNTPVKL 126
 DB 85 YVNFQDNLDLIPVENELEFVDSYKPGLSYAANPEAEESLIPLKEAVNVVVSQOPNTPVKL 144
 QY 127 PVKLGATAGTGLRLEGAENIIQAVRDMLSNRSALNVQSDAVSILDGTORGXYLMTIN 186
 DB 145 PVKLGATAGTGLRLEGAENIIQAVRDMLSNRSALNVQSDAVSILDGTORGXYLMTIN 204
 QY 187 LCKRFTKTVGVVDLGGGSVQMTYAVSRNTAKNAPVPEGEDPYIKKLVLOGKKYDLVHS 246
 DB 205 LCKRFTKTVGVVDLGGGSVQMTYAVSRNTAKNAPVPEGEDPYIKKLVLOGKKYDLVHS 264
 QY 247 YVNSYLRYGAEARERAFEFVAGSAPNCILAGDGAITYTSGAATKASAPASGSLNOCRIATK 306
 DB 265 YVNSYLRYGAEARERAFEFVAGSAPNCILAGDGAITYTSGAATKASAPASGSLNOCRIATK 324
 QY 307 IALKALV-NAPCPYONCTFGGIMNGGGSGQKNLFLTSSFYLSSEVGIFFV--KPNAKIRPV 363
 DB 325 IALKALV-NAPCPYONCTFGGIMNGGGSGQKNLFLTSSFYLSSEVGIFFV--KPNAKIRPV 383
 QY 364 IRPVDLTKAALACKTNLEDAKSKYIPDLKESVEVCLDLYVYLLVDGFGLDPPQEVTVAN 423
 DB 384 IRPVDLTKAALACKTNLEDAKSKYIPDLKESVEVCLDLYVYLLVDGFGLDPPQEVTVAN 442
 QY 424 TVANEIEYODALVEAAMPPLGTAIEAISS 451
 DB 443 TVANEIEYODALVEAAMPPLGTAIEAISS 470

RESULT 14
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 AC 09M7B3;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE APYRASE.
 GN ATAPY2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

RESULT	15	
09AUI4		
ID	09AUI4	PRELIMINARY; PRT; 326 AA.
AC	09AUI4;	
DT	01-JUN-2001 (TREMBLrel. 17, Created)	
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	PUTATIVE APYRASE (FRAGMENT).	
GN	APY4.	
OS	Medicago truncatula (Barrel medic).	
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae	
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.	
OX	NCBI_TaxID=3880;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=ROOT;	
RX	MEDLINE=21196009; PubMed=11299390;	
RA	Cohn J.R., Uhm T., Ramu S., Nam Y.W., Kim D.J., Penmetsta R.V., Wood T.C., Denny R.L., Young N.D., Cook D.R., Stacey G.;	
RT	"Differential regulation of a family of apyrase genes from Medicago truncatula.";	

Search completed: June 28, 2002, 04:06:00
Job time: 378 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 01:31:50 ; Search time 2851 Seconds
(without alignments)
10929.363 Million cell updates/sec

Title: US-09-657-631-8
Perfect score: 1489
Sequence: 1 aagtgctctctctctctgtag.....cgcattcttctctcttctt

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: GenEmbl:*
2: gb_ba:*
3: gb_hcg:*
4: gb_in:*
5: gb_cm:*
6: gb_ov:*
7: gb_pat:*
8: gb_ph:*
9: gb_pl:*
10: gb_pr:*
11: gb_ro:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
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16: em_fun:*
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18: em_in:*
19: em_mu:*
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26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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1	1489	100.0	1489	8	AF156780	Lotus jap
2	889.8	59.8	1463	8	AF207688	Glycine s
3	876.8	58.9	1401	8	AF288132	Medicago
4	869.2	58.4	1460	8	AF156782	Medicago
5	844.6	56.7	1648	8	AB027613	Pisum sat
6	844.6	56.7	1651	8	AB038668	Pisum sat
7	839.8	56.4	1572	8	AB027614	Pisum sat
8	839.8	56.4	1645	8	AB022319	Pisum sat
9	839.8	56.4	1648	8	AB038669	Pisum sat
10	839.8	56.4	1661	8	PSMTPEASE	
11	835	56.1	1667	6	E51056	
12	833.4	56.0	1697	6	E51055	
13	830.4	55.8	1368	6	E51054	
14	830.4	55.8	1557	8	AB027616	Pisum sat
15	824.6	55.4	1608	8	AF139807	Pisum sat
16	782.4	52.5	1423	8	AB027615	Pisum sat
17	665.6	44.7	1395	8	AF207687	Glycine s
18	652.4	43.8	1435	8	AF156781	Dolichos
19	630	42.3	1060	8	AF288133	Medicago
20	628.2	42.2	1790	8	AF305783	Pisum sat
21	500.4	33.6	1827	8	AF141671	Arabidops
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24	441.4	29.6	1530	8	STU58597	Solanum tub
25	250	16.8	2216	8	AB023621	Pisum sat
26	250	16.8	2350	8	AB038554	Pisum sat
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28	194.4	13.1	751	8	AB032754	Solanum m
29	115.8	7.8	620	8	AB030444S1	Pisum sat
30	112.2	7.5	100814	2	AP003929	
31	110	7.4	584	8	AB030444S2	Pisum sat
32	106.6	7.2	83948	8	AB012246	Arabidops
33	97.2	6.5	1900	8	AF465240	Schizosac
34	97.2	6.5	21917	8	SPAC824	
35	97	6.5	1800	8	CAL421721	S.pombe c
36	93.8	6.3	110804	8	ATAC016829	Candida a
37	93.2	6.3	1633	10	MMU238636	Mus muscu
38	93.2	6.3	1939	10	AF136571	Mus muscu
39	93.2	6.3	2099	10	BC015247	Mus muscu
40	93.2	6.3	2119	10	AF006482	Mus muscu
41	91.2	6.1	1998	9	AF039918	Mus muscu
42	91.2	6.1	2033	9	AF136572	Homo sapi
43	91.2	6.1	3157	9	BC020966	Homo sapi
44	85.6	5.7	1749	10	AF084568	Mesocric
45	85.6	5.7	1750	10	AF084569	Mesocric

ALIGNMENTS

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LOCUS		AF156780				
DEFINITION		Lotus japonicus nod factor binding lectin-nucleotide				
ACCESSION		AF156780				
VERSION		AF156780.1	GI:6006794			
KEYWORDS						
SOURCE		Lotus japonicus				
ORGANISM		Lotus japonicus				
REFERENCE		1 (bases 1 to 1489)				
AUTHORS		Roberts,N.J., Brigham,J., Wu,B., Murphy,J.B., Volpin,H., Phillips,D.A. and Etzler,M.E.				
TITLE		A nod factor-binding lectin is a member of a distinct class of apyrases that may be unique to the legumes				
JOURNAL		Mol. Gen. Genet. 262 (2), 261-267 (1999)				
MEDLINE		99444909				
PUBMED		10517321				
REFERENCE		2 (bases 1 to 1489)				

REFERENCE	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	FEATURES				
1	(bases 1 to 1463)	Day, R.B., McAlvin, C.B., Loh, J.T., Denny, R.L., Wood, T.C., Young, N.D.	Differential expression of two soybean apyrases, one of which is an early nodulin	MoJ. Plant Microbe Interact. 13 (10), 1053-1070 (2000)	11043467	2 (bases 1 to 1463)	Day, R.B., McAlvin, C.B., Loh, J.T., Fink, S.E., Denny, R.L., Dunlap, J., Young, N.D., and Stacey, G.				
2	(bases 1 to 1463)	Young, R.B., McAlvin, C.B., Loh, J.T., Fink, S.E., Denny, R.L., Dunlap, J., Young, N.D., and Stacey, G.	Direct Submission	Submitted (21-NOV-1999)	Microbiology, The University of Tennessee, M409 Walters Life Science Building, Knoxville, TN 37996-0845, USA	Location/Qualifiers	1. .1463				
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5	BASE COUNT	417 a	301 c	324 g	421 t						
6	ORIGIN										
7	Query Match	59.8%;	Score 889.8;	DB 8;	Length 1463;						
8	Best Local Similarity	79.6%;	Pred. No. 9.6e-199;								
9	Matches 1105;	Conservative	0;	Mismatches 272;	Indels 12;	Gaps 4;					
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11											
12	Db	40	GGACTAAGACATGACCTCTTCCCTTAACCCCTTCCTACTCTTCTACTCTTGATTCATTCAAA	99							
13	89	ctgcatctcttctcccaatatatctcggaaacaacatctcatgtaatgtaagataatc	148								
14											
15	Db	100	CAGACTCTCTCTTACCCCAATATCATCTGATGAGACATCTTACTCATCTCATGTAAGATCT	159							
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17											
18	Db	160	TCCCCAAA---CAGAACCTATACACCTGCTAGACGCTGTATCTTTATGCTGTAGACACTG	216							
19	209	gaagcagatcactgctcacaatttgatcagaaacttagatctcctccggttgaaacg	268								
20											
21	Db	217	GTACCGGTGCATCTCTTCCTTCCGACACCAAGAACTTGATGATCTCTGATTTGGCAACG	276							
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24	Db	277	AACTGAGATTTTATATAGGTAAACACCCGGTTTATAGTACATGACAGATATATCTTCAAC	336							
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26											
27	Db	337	AAGCTGAGAAATCTTTATCCACCTTTTAAAGAGAAAGCTTGAAGGTGTGTGCTCTGAGAC	396							
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Db	457	ATGCTTGTGAAGAGATATTTCACAGCGGTAGAGATTTCGTCAAGAAACAAATACCTCGA	516
Qy	509	atgttcaacacagatgcatctatctctgtatgaaacccaagaaggtcttactcttggg	568
Db	517	ACGCTTCAACCAAGATGCGTGTGATATTATTGATGCAACCCAAAGAGTCTTATCTATGGG	576
Qy	569	tgaacataactactctctcttggggaagtgtggaaaagatttccaaagcagtggaagtag	628
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Qy	629	ttgacccaaggatggtggtcaggtgcaaatgacatatactcaatctccaaagaaacagctataaa	688
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Db	937	ATGAAATATAGAGAGTGTGTTCTTCAAGCTCTCAAAATTAATGATGATGCAATGCCCCATCAAA	996
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Qy	1226	gcttgagatctgtctacaggtgtatacaatctgcttgtatgataattgtgtcttgatccatttc	1289
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Qy	1286	aagaaggttacaagtgtgcaatgaaatgtgaatatcagaatgctctgtgtggaagcgcgaatgc	1345
Db	1294	AAGAGATTTACAGTGGCGAAATGAATATGAAATATACAGATGCTCTTGTGMAAGTGCATGCG	1353
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Db	1414	TTATTTAAA 1422	

AF288132 LOCUS AF288132 1401 bp mRNA linear PLN 27-APR-2001
 DEFINITION Medicago truncatula putative apyrase (apy1) mRNA, complete cds.
 ACCESSION AF288132
 VERSION AF288132.1 GI:13183348
 KEYWORDS
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
 REFERENCE 1 (bases 1 to 1401)
 AUTHORS Cohn, J., Denny, R., Uhm, T., Ramu, S., Nam, Y.W., Kim, D.J., Pennetsa, R.V., Wood, T.C., Denny, R.L., Young, N.D., Cook, D.R. and Stacey, G.
 TITLE Differential regulation of a family of apyrase genes from Medicago truncatula
 JOURNAL Plant Physiol. 125 (4), 2104-2119 (2001)
 MEDLINE 21196099
 PUBMED 1129390
 REFERENCES 2 (bases 1 to 1401)
 AUTHORS Cohn, J., Ramu, S., Uhm, T., Nam, Y.W., Kim, D.J., Pennetsa, R.V., Cook, D., Denny, R., Young, N. and Stacey, G.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUL-2000) Microbiology, University of Tennessee, M409
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 BASE COUNT 420 a 251 c 298 g 432 t
 ORIGIN

Query Match 58.9%; Score 876.8; DB 8; Length 1401;
 Best Local Similarity 77.9%; Pred. No. 1,1e-195;
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QY	1342	169cctcttagagcagccgcoltagaacatatacatatcattgcccctaattttagagatcatc	1401
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QY	1402	tatttatttaa	1413
DB	1390	tattttgttttaa	1401
RESULT	4		
LOCUS	AF156782	1460 bp	linear
DEFINITION	Medicago sativa nod factor binding lectin-nucleotide phosphohydrolase (LNP) mRNA, complete cds.		PLN 09-NOV-1999
ACCESSION	AF156782		
VERSION	AF156782.1	GI:6006798	
KEYWORDS			
SOURCE	Medicago sativa.		
ORGANISM	Medicago sativa.		
REFERENCE	1 (bases 1 to 1460)		
AUTHORS	Roberts,N.J., Brigham,J., Wu,B., Murphy,J.B., Volpin,H., Phillips,D.A. and Etzler,M.E.		
TITLE	A Nod factor-binding lectin is a member of a distinct class of apyrases that may be unique to the legumes		
JOURNAL	Mol. Gen. Genet. 262 (2), 261-267 (1999)		
MEDLINE	99444909		
PUBMED	10517321		
REFERENCE	2 (bases 1 to 1460)		
AUTHORS	Roberts,N.J., Brigham,J., Wu,B., Murphy,J.B., Volpin,H., Phillips,D.A. and Etzler,M.E.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-JUN-1999)		
FEATURES	Molecular and Cellular Biology, University of California, Davis, 1 Shields Avenue, Davis, CA 95616, USA		
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Qy	211	agcagatgccatgltctaaatttttgaacgaactagatctcttccgtttgaaacga	270
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Qy	271	cttagatttatgatttcgtgtaaacccggttttagtctaaagctcgtcaatcttgaaga	330
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Db	853	CATATCAATATTCAGGAGAAGACTTTAAGGCACACTGCTTACACTTGTGGTCAAACTTAA	912
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OY	990	ttgcacctttggttggaatalgaagacggttggaagtggtgcataaaaactcttccot	1049
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OY	1050	tacttcactcttctcatcttaccctctcgtgaagatgttggatcct---tgtgaataaaccaa	1106
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DEFINITION	Pisum sativum mRNA for apyrase, complete cds, clone:pkS17-2.		
ACCESSION	ABO38668		
VERSION	ABO38668.1	GI:11596080	
KEYWORDS	aprase.		
SOURCE	Pisum sativum (strain:Alaska) Seedling Dark grown stem internode CDNA to mDNA, clone_1.jp:pea internode cDNA library clone:pkS17-2.		
ORGANISM	Pisum sativum		
REFERENCE	1 (sites)		
AUTHORS	Shibata,K., Abe,S. and Davies,E.		
TITLE	Structure of the coding region and mRNA variants of the aprase from Pisum Sativum		
JOURNAL	Acta Physiol. Plant. 20, 3-13 (2001)		
REFERENCE	2 (bases 1 to 1651)		
AUTHORS	Shibata,K. and Abe,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-FEB-2000) Shunosuke Abe, Ehime University, College of Agriculture; Tatumki 3-5-7, Matsuyama, Ehime 790-8566, Japan (E-mail:abe@nch.abr.ehime-u.ac.jp, URL:http://web.mcb.abr.ehime-u.ac.jp, Tel:+81-89-946-9853, Fax:+81-89-946-9853)		

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DEFINITION Pisum sativum mRNA for apyrase, complete cds.
 ACCESSION AB022319
 VERSION AB022319.1 GI:4519172
 KEYWORDS apyrase.
 SOURCE Pisum sativum (cultivar:Alaska) seedling dark grown stem internode
 ORGANISM Pisum sativum
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 REFERENCE 1 (sites)
 SHIBATA,K., Abe,S. and Davies,E.
 TITLE Structure of the coding region and mRNA variants of the apyrase from Pisum Sativum
 JOURNAL Acta Physiol. Plant. 20, 3-13 (2001)
 REFERENCE 2 (bases 1 to 1645)
 JOURNAL Shibata,K. and Abe,S.
 TITLE Direct Submission
 JOURNAL Submitted (12-JAN-1999) Shunnosuke Abe, University of Ehime, Department of Biological Resources; 3-5-7 Tarumi, Matsuyama, Ehime 790-8506, Japan (E-mail:abe@pc.ehime-u.ac.jp), URL:http://web-mcb.agr.ehime-u.ac.jp/dunnshl/, Tel:81-899-46-9853, Fax:81-899-46-9853)
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DEFINITION Pisum sativum mRNA for apyrase, complete cds, clone:PKS30-3.
ACCESSION AB038669
VERSION AB038669.1 GI:11596082
KEYWORDS apyrase.
SOURCE
ORGANISM Pisum sativum (strain:Alaska) Seedling Dark grown stem internode
CDNA to mRNA, clone.lib:pea Internode cDNA library clone:PKS30-3.
Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.
REFERENCE 1 (sites)
AUTHORS Shibata,K., Abe,S. and Davies,E.
TITLE Structure of the coding region and mRNA variants of the apyrase
from Pisum Sativum
JOURNAL Acta Physiol. Plant. 20, 3-13 (2001)
AUTHORS 2 (bases 1 to 1648)
Shibata,K. and Abe,S.
DIRECT SUBMISSION
SUBMITTED (22-FEB-2000) Shunnosuke Abe, Ehime University, College
of Agriculture; Tarumi 3-5-7, Matsuyama, Ehime 790-8566, Japan
(E-mail:abe@mb.agr.ehime-u.ac.jp,
URL:http://web-mcb.agr.ehime-u.ac.jp, Tel:81-89-946-9853,
Fax:+81-89-946-9853)

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ORIGIN

Query Match 56.4%; Score 839.8; DB 8; Length 1648;
Best Local Similarity 76.2%; Pred. No. 5,3e-187;
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.
1 (bases 1 to 1661)
Hsieh, H.L., Tong, C.G., Thomas, C. and Roux, S.J.
Light-modulated abundance of an mRNA encoding a
calmodulin-regulated, chromatin-associated NTPase in pea
Plant Mol. Biol. 30 (1), 135-147 (1996)
96197404
2 (bases 1 to 455)
Hsieh, H. and Roux, S.J.
Cloning of the cDNA and expression of the mRNA for a gene encoding
a calmodulin-regulated nucleoside triphosphatase associated with
the envelope of pea nuclei
Unpublished
3 (bases 1 to 1661)
Direct Submission
Submitted (21-Apr-1994) Hsieh H., University of Texas at Austin,
Botany, Biological Lab. Rm 6, Austin, Texas, USA, 78713
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Matches 1062; Conservative 0; Mismatches 322; Indels 9; Gaps 2;

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E51056 Disease resistant polypeptide, disease resistant gene, method for
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transfomed plant, and nucleotide triphosphate hydrolase.
ACCESSION
E51056
VERSION
JP 2001017176-A/3.
KEYWORDS
unidentified.
SOURCE
unclassified.
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 1667)
AUTHORS
Shiraiishi,T. and Furusawa,I.
TITLE
Disease resistant polypeptide, disease resistant gene, method for
imparting disease resistance to plant, disease resistance-imparted
transfomed plant, and nucleotide triphosphate hydrolase
JOURNAL
Patent: JP 2001017176-A 3 23-JAN-2001;
PRESIDENT OF KYOTO UNIVERSITY
OS
Pisum sativum L. (Garden Pea)
PN
JP 2001017176-A/3
PD
23-JAN-2001
PF
02-JUL-1999 JP 1999189129
PR
TOMONORI SHIRAIISHI,IWAO FURUSAWA
PI
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Location/Qualifiers
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KEYWORDS	Disease resistant polypeptide, disease resistant gene, method for imparting disease resistance to plant, disease resistance-imparted transformed plant, and nucleotide triphosphate hydrolase.
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VERSION	E51055.1 GI:18629461
KEYWORDS	JP 2001017176-A/2.
SOURCE	unidentified.
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 1697)
AUTHORS	Shiraishi, T. and Furusawa, I.
TITLE	Disease resistant polypeptide, disease resistant gene, method for imparting disease resistance to plant, disease resistance-imparted transformed plant, and nucleotide triphosphate hydrolase
JOURNAL	Patent: JP 2001017176-A 2 23-JAN-2001;
COMMENT	PRESIDENT OF KYOTO UNIVERSITY OS Pisum sativum L. (Garden Pea) PN JP 2001017176-A/2 PD 23-JAN-2001 PF 02-JUL-1999 JP 1999189129 PR PI TOMONORI SHIRAISHI, IWAO FURUSAWA PC C12N15/09, A01H5/00, C07K14/415, C12N9/16, C12N15/00 CC FH Key Location/Qualifiers FT 1.1697 FT source /organism='Pisum sativum L. (Garden Pea)'. FT location/Qualifiers 1.1697 /organism='unidentified' /db_xref='taxon:32644'
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	ORGANISM	unclassified.		
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DEFINITION	Pisum sativum mRNA for apyrase, partial cds, clone:pms3-3.
ACCESSION	AB027616
VERSION	AB027616.1
KEYWORDS	GI:6683665 apyrase, -

SOURCE	Pisum sativum (strain:Alaska) Seedling Dark grown stem internode
ORGANISM	CDNA clone_11b:pea internode cdna library clone:pk3-3.
	Pisum sativum

REFERENCE
AUTHORS
1 (bases 1 to 157)
Shibata, K. and Abe, S.

JOURNAL REFERENCE AUTHORS TITLE JOURNAL	Published Only in Database (2000) In press 2 (bases 1 to 1557) Shibata, K. and Abe, S. Direct Submission Submitted (24-MAY-1999) Shunnosuke Abe, University of Ehime,
---	---

JOURNAL Submitted (24-MAY-1999) Shunosuke Abe, University of Ehime,
Department of Biological Resources, 3-5-7 Tarumi, Matsuyama, Ehime
790-8566, Japan (E-mail: abedp@ehime-u.ac.jp,
URL: <http://web-mcb.agr.ehime-u.ac.jp/bunnsh/>, Tel: 81-899-46-9853,
Fax: 81-899-46-9853)

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 AF139807.1 GI:4868374
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 Dolichos.
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 Etzler,M.E., Kalsi,G., Ewing,N.N., Roberts,N.J., Day,R.B. and
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 A nod factor binding lectin with apyrase activity from legume roots
 JOURNAL
 Proc. Natl. Acad. Sci. U.S.A. 96 (10), 5856-5861 (1999)
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 Etzler,M.E., Kalsi,G., Ewing,N.N., Roberts,N.J., Day,R.B. and
 Murphy,J.B.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (31-MAR-1999) Molecular and Cellular Biology, University
 of California, Davis, 1 Shields Avenue, Davis, CA 95616, USA
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 04:00:36 ; Search time 37.72 Seconds

(without alignments)
1176.916 Million cell updates/sec

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Scoring table: BLOSUM62
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Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	540	22.7	556	2	probable guanosine
4	478.5	20.1	479	2	hypothetical prote
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40	100	4.2	526965	2	NADH oxidase - Ent
41	100	4.2	537	2	probable binding p
42	100	4.2	1204	2	probable pyrolysin
43	99.5	4.2	342	2	dihydroxyacetone k
44	99.5	4.2	498	2	glycerol kinase, G
45	99.5	4.2	677	2	hypothetical prote

ALIGNMENTS

RESULT 1

S48859
nucleoside triphosphatase precursor, chromatin-associated - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Sep-1999
C:Accession: S65147; S48859
R:Hu, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
Plant Mol. Biol. 30, 135-147, 1996
A:Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin-associated
A:Reference number: S65147; MUID:96197404
A:Accession: S65147
A:Molecule type: mRNA
A:Residues: 1-455 <HS2>
A:Cross-References: EMBL:Z372743; NID:9563611; PIDN:CA83655.1; PID:9563612
C:Superfamily: nucleoside triphosphatase Chromatin-associated
C:Keywords: nucleus

Query Match	70.3%	Score 1675.5;	DB 2;	Length 455;
Best Local Similarity	68.7%	Pred. No. 4.3e-115;		
Matches 314;	Conservative 64;	Mismatches 76;	Indels 3;	Gaps 2;
QY	7	MDFLISLMTFVEMLMPAIISSOYLGNINILMKRILPKNOEPTVSYAVIFDAGSTSRVH	66	
DB	1	MELLILITFLFSPALITSSOYLGNILTSKIFL--KOEISSTAVVPDAGSTSRH	58	
QY	67	VYVFNQNDLPLPYENLEFEYDYSVPGIASSYANPEEAESLIPLEAEVNVVPSOQPT	126	
DB	59	VYVFNQNDLPLHKGVEYYNKTTPGLSSYANPEQAASLIPLEAEVNVVPSOQPT	118	
QY	127	PKVLGATAGLRLEGNAAENILQAVDMLSNRKALVQSDAVSILDTGEGSLMTWTNY	186	
DB	119	PVRLGATAGLRRLNGDASEKIILOSVDMLSNRSTFVQPDVAVSIIDTGEGLMTWTNY	178	
QY	187	LGKLGKRFKTYGVVDLGGGSVQMTYAVSRNAKNAKPYEEDDPYIKKLVLOGKKYD	246	
DB	179	ALGNLKKRTTYGVVDLGGGSVQMTYAVSRNAKNAKPYEEDDPYIKKLVLOGKKYD	238	
QY	247	VYHSYLRYGREAIFRAEIFFVAGGSANPCILAGFDGAYTTSYGAERYAPASAPASNLQCKR	306	
DB	239	VYHSYLHFRERASRAELIKLTPRSPNCLLAGNGIYTSYGEFKATVATSGANFKCKN	298	
QY	307	IALKALKVNAPCPYONCTGCGIYNGGSGGOKKFLTSSRYIYSEVG--IFVKKPAKIR	365	
DB	299	TIRKALKVNAPCPYONCTGCGIYNGGSGGOKKFLTSSRYIYSEVG--IFVKKPAKIR	358	
QY	366	PVDLKAALACKTNEDKSKYPDLVYKDSVEYVCLDLYVYVTLVLDGSDPPEVNY	425	
DB	359	PVDLKAALACKTNEDKSKYPDLVYKDSVEYVCLDLYVYVTLVLDGSDPPEVNY	418	
QY	426	ANEIEYODALVEAAMPDLGTAIEAIISSLPKFERLMYFI 462		


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Db 207 SLGGPRLKTTGIVELGGSAAQVTFYSS-----PMPE-----PSRTISFGNWTYNLXSH 256
Qy 250 SYLRGR-----EAPRAEIFKVAGSGANPCIIAGFD-GAYTYS-- 286
Db 257 SFLHGGQAAMDKLWGLSLSRDHSNAGSEPTREKIF-----TDPCAPRGYNLDANTOKHL 310
Qy 287 -----GAEKVS-APASGSNLNOCRIALKAALKVNAPCPYONCTFPGIINNGGSGSQKLF 341
Db 311 SGLLAEBERLSDFOVAGSNYSOCSRSAULTILO-----DGNG----RILI 350
Qy 342 LTSSFYYLSDEVDGIFFVNKPARKIRPVDLKTAACKTNLEDAKSRYDLYEKKDSVEYVC 401
Db 351 ILAGSFLFFELG-----EKAMLNSMISAGERCCGEDMSKLKRVKDPDSLHEEDLLRF-C 402
Qy 402 LDLYVVYTYTLVADGCLDFPFGEVTYANLEIEYODALYEAMPICATAIE 447
Db 403 FSSAATVSLDLDTLGI-PLDDIRIGVANQAGD-IPLDMALGAFTQ 445
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RESULT 9
E86276
hypothetical protein F14L17.1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: E86276
R:Proteoglis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzalli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: E86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <STO>
A:Cross-references: GB:AE005172; NID:97262666; PIDN:AAF43924.1; GSPDB:GN00141
C:Genetics:
;Map position: 1

Query Match	15.9%;	Score 379;	DB 2;	Length 405;
Best Local Similarity	27.6%;	Pred. No. 4.4e-20;		
Matches 116;	Conservative 71;	Mismatches 161;	Indels 72;	Gaps 18

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Oy 56 FDAQSGRVHVVNDQDLDPVENELEFYDSVK--PGLSSYANPEEAESLILPLKE 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 FESGKP-----VDFDGE-----EHYASLKLSTGSLSTADNPBGASVYTKLEEF 51

Oy 114 AENVVPSQOPNTPVKLGATAGLRLLGCGMAENILQAVRDL,SNRSALNVQSDAYSILDG 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 52 AKGRIPKRLKKSIDIRLMATAGMRLLDPVQEOILIDVTRVLR--SGEKFODEMATVISG 110

Oy 174 TOEGSYLVVNTNLLGKRGKRFRTKTVGVYDGGGCVQMTYAVSRRTANAKRPVGEDPY 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 TDEGTYAMVYANHALGSLGSDPLKTTGIVELGASAOVTPESEH-----VP-----Pe 159

Oy 234 IKKLVLQCK-KYDLVHSLYLRGREAFAETIFK-----VAGGSA----NPCIILAGF-- 279
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 FSRRTSYGNVSYTYTSHSFLDFGQDAADKLESLQNSVAASTGCDIVEDCTPFGYIYD 219

Oy 280 -----DGATYVYSGAEVYSAPA--SGSNLNOCRKLTALALVYNAF-CYONCTPEGGIN- 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 220 THSQKSDSGFLSEBEKFKASLQVQAAGDPTKCRSRTLMLDGBKNCAYKHCISGISTTP 279

Oy 331 --GGGSGSQKNLUTSSFYVYLEDVGIFVKNRPNAKIRPVDLTKTAALACKTNLEDAKSY 388
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 280 NIOGSLFATNEFPHFKSGFFGJGKEKEML-----SEMILGKRFCCGEMSKLKERKY 328

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Qy 389 PDLYEKDSVEVCLDLYVYVTLVLVDGEG--LDPEQEVTVANEIEYODALVEAMPGLGTAI 446

Db 329 PTYKDKYLHRY-CFSSAYIISMHDSGLVALDD-ERIKVASKAKGEN--IPUDWALGAFI 384

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RESULT 10
T40856
probable nucleotide phosphatase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40856
R:Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21952
A:Accession: T40856
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-572 <RAM>
A:Cross-references: EMBL:AL121783; PIDN:CAB57847.1; GSPDB:GN00068; SPDB:SPCC11E10.05C
A:Experimental source: strain 972h; cosmid c11e10
C:Genetics:
A:Gene: SPDB:SPCC11E10.05C
A:Map position: 3

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Query Match	15.9%	Score 379;	DB 2;	Length 572;
Best Local Similarity	28.2%	Pred. No. 7.4e-20;		
Matches 136;	Conservative 68;	Mismatches 176;	Indels 102;	Gaps 21

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QY      49 VTSVAVIFDAGSTGSRHVVNDQNDL-----LLP-VENEL-----EFLDSVKPLGLSS 95
      | : |||:| :| :| : || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      2 VRKYGIFIDAGSSGSRLLIYSNDYDTPSSLSDKYKLLPIETGIDGGKWSLKVQPGISS 61

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QY 96 YAANPEEAAS-LIPILKKAENVVPVSQQNTPKLGATAGRLLEGNAENILQAVRDM 154
 :| | : | | : :| | | | | | :|
 Db 62 FANNPKHVGGKHLKELIDFAAAHAI PKDVHKETPYFLSATAGMRLLGVDAAQNKILSHACRY 121

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qy      135 LSNRSALNVC--SDAVALDGGEGSYMTVINTLLGDKRFRTKIVGVVDJGGGSQOMI 212
          :   :: |::: ::| | | | |::| | | | |::| | | | |::| | | | |
Db      122 IKKNYDFIDPNCNSIRVIDGAEGMYGLATINILKLTLEEKDTSTVGFLDMGGASVOIA 189

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213 IAVSNINANNPNVAFESDEFTANLV-----GGANLIDIVISILNIG KEGN 200
      ::::| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 182 FELPSSQLKN-----YKDSISYHIGLNGQQLLEPLFVITWLGFGANEAYRRL 231

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Db 285 KPCSMDCNFDGISIPVDFANTEVGVSEFWYINDVFDMGSGYHFPNF--YKKVD---- 339

340 --EYCGTEWETMLSR---LYNKELTPSIDENKLEKLCFKASWALNVLHEGFDVPKSNTSS 394

Db 395 NDAKDGLSVIPAYHSPF---TSLEKIE----RTEVSWTLCGOVLLYASNOQLLAKPEYANY 447

Db	448	YM	449
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RESULT 11
T16696
hypothetical protein R07E4.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16696
R:Miller, N.

submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid R07E4.

A:Reference number: Z18561

A:Accession: T16966

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-557 <M1>

A:Cross-references: EMBL:039652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:R07E4.4

A:Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2

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Query Match          15.9%; Score 378.5; DB 2; Length 557;
Best Local Similarity 27.7%; Pred. No. 7.7e-20;
Matches 125; Conservative 70; Mismatches 190; Indels 67; Gaps 17;

QY 51 SYAVIFDAGSTGSRVHYVNFQNDLLPVENLEFYDS-----VKPGLSSYANPEEA 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43 SYGVICDAGSTGTRLEFVNMISTSDSELTQLEPVYIDNKPVMKISPGLSTFGTKPAQAA 102

QY 105 ESILPLKEAENVVPSOQPNTPVKLGATAGRLLEG-----MAENILOAVRDMLSRS 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 EYLRPLMEIAERHIEDEKRPITPVIFATAGRLIPDEYVLIGQKAVLKNLRNLPKIT 162

QY 160 ALNVOSDAVSIIDGQEGSYLWNTINYLGLKGRFT-----KTVGVDLGG 206
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 163 SMQVLEKEHRIIEGKMEGIYSWIAVNALGKFNKTALDPGTPSAHAKQKTVGGLDGG 222

QY 207 GSVQMTYAVSRN---TAKNAPKVRPG--EDPYIKLVLOGKKYLVHYSYLRG-REAFR 260
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 ASAQIAFELPDTDSFSJINVENINLGCREDLSL-----FKYKLFVTFFGYGVNEGIR 275

QY 261 -----AEIFVYAGGSA--NPCILAGFDGAYTYSGAEKYVAPASGSLNOCRIKALAL 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 276 KYEHLMLSKLDQNGTGIQDDCMPLNKHKTVLENGENFVR--KGTGMWNTCSNEVKKL 333

QY 313 KVNAP---CPYQ--NCTGGJINNGGGSGQKNLFLTSSFYLSBDV-GIFVKNKPNKATRP 366
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 334 NPESSEYCKAEAKCYGAAPAPASIPLSNIEMYGFESEYWSYTHDVLGLGQYDAENIAK 393

QY 367 VDLKTAACKTNLEDAKSKYPLDYERDSVEYVCLDLYVYTTLLVNGFGD---FPQE 422
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 394 KTOQYCSKRNSTIOAESKKQLYPPA-DEERLRTQCFKSAMITTSVLHDGFSVDKTHNRFQS 452

QY 423 V-TVANEIEYDQALVEAAMPGLGTAIEAISLP 453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 453 VSTIAGQ-----EYQWALGAMITYHMRFPF 476

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RESULT 12

T34147 hypothetical protein C33H5.14 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Mar-2000

C:Accession: T34147

R:Bradshaw H.; Stellyes, L.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid C33H5.

A:Reference number: Z21482

A:Accession: T34147

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-485

A:Cross-references: EMBL:U41007; PIDN:AAA82272.1; CESP:C33H5.14

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:C33H5.14

A:Introns: 22/1; 83/1; 120/2; 167/1; 269/3; 399/3

C:Superfamily: nucleoside triphosphatase chromatin-associated

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Query Match          15.7%; Score 375; DB 2; Length 485;
Best Local Similarity 26.6%; Pred. No. 1.1e-19;
Matches 122; Conservative 73; Mismatches 183; Indels 80; Gaps 18;

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QY 38 RKILPKNOEVTSTAVIFDAGSTGSRVHYVNFQNDLLPVENLEFYDSVKR 91
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 14 RSVYETKNN---IKGVICDAGSGGTRLPFYTLKPLSGGLNIDTLTHESE-PVKKVTP 69

QY 92 GLSSYANPEEAASLPLKAEENVVPSOQPNTPVKLGATAGRLLEGNAENILOAV 151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 GLSFGDKPEQVEYELPLPFAEHIPIYQELGETDLLIFATAGMRLLPAAQDAITKNL 129

QY 152 RDMLSNRSALNVOSDAVSIIDGQEGSYLWNTINYLGLKGRFTKTVGVVDLGGSSVM 211
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 QNGKSYTALRVSDSNIRITIDGANEGLYSWIAVNYLIGRDKDNDSKVMGMDGASVOT 189

QY 212 TYAVSRNTAK-----NAPKVEGEDPYIKLVLOGKKYLVHYSYLRG---EA 258
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 AFEIANEKESYNGGVNVEINLGSJETNED-----KYKIYSTPLTGYANGLAK 239

QY 259 FRAIFVYAGGSANPCLAGFD---GAYTYSG-AEKYVAPASGSLNOCRIKALALV 314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 240 YENSLVR-SGNSNDSCSPRLNRLIGFTVNGEVDVCLAQVSLIGD-----KA 289

QY 315 NACPYNCTFGGJINNGGGSGQKNLFLTSSFYLSBDV---IFVKNKPNKATRPVDLK 370
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 290 QPSCPNTCFLRVNIAVSVNLSTVOLYGESEYVITTSNFGSGGEHYQKFTDVKRY--- 346

QY 371 TAACKTNLEED-----AKSKYPLDYERDSVEYVCLDLYVYTTLLVDFGIDP---PQ 421
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 347 -----CQKDMNDIODGFKNRFPNA-DIERLTGNCFKAAWTSVYLDGFNDKTHLEQ 399

QY 422 EV-TVANEIEYDQALVEAAMPGLGTAIEAISLPKFERL 458
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 400 SVLKINGE-----EKQWALGAMLYHSKDL-KENLL 428

```

RESULT 13

S50463 hypothetical protein YER005w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001

C:Accession: S50463

R:Dieckrich, F.S.

submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lamb

A:Reference number: S50433

A:Accession: S50463

A:Molecule type: DNA

A:Residues: 1-630 <DIE>

A:Cross-references: EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005; MIPS:YER005

C:Genetics:

A:Gene: MIPS:YER005w

A:Map position: 5R

```

Query Match          14.4%; Score 343.5; DB 2; Length 630;
Best Local Similarity 24.3%; Pred. No. 3.4e-17;
Matches 112; Conservative 78; Mismatches 177; Indels 93; Gaps 16;

```

```

QY 52 YAVITFDAGSTGSRVHYVNFQNDLLPVEN-----ELFFYDSVKRGLSSY 96
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 10 FGVIVDAGSSGSRHIFKWDQTESLHATNDSQSIILQSVPHIQEKDMTFKLNPGJSSF 69

QY 97 AANPEEAESLI-PLKKEENVVPSOQPNTPVKLGATAGRLLEGNAENILOAVRDM 155
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 EKKPDATKSHTKPLDPRKNITIPESHWSGCVFQATAGMKLLPQDIQSSILDLQGL 129

QY 156 SNRSALNQ--SDAVSIIDGQEGSYLWNTINYLGLG-----KLGRFTTVGVVDLGG 206
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 KHPAFELVEDCSAQIQVIDGETEGLYGMLGLNLYLGHNDVNPVSDHF--TFPFMDMG 187

QY 207 GSVQMTYAVSRNTAKNAKVPBEGDP---YIKKLVLOGKKYLVHYSYLRG---REA 258

```

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Db 188 ASQQLAFA-----PHDSGEIARHHDIAITFLRSVNGDLQKMDVEFVSTWLGCGANQARR 242
Oy 259 FRAEIKVAGGSAN-----PCIIAGFDGATTSYGAEEKVAPASGSLUNC 304
Db 243 YLAQQLINTLPENTINDYENDDFSTRNLNDCMPRGSSSTDEFFDITFIH--AGSGVYECG 299
Oy 305 RKIALKALKVNAPCPYONCTPGGIMNGGSGOKNLFTRSSPYLYSEDEVGIFVKNPKNAKI 364
Db 300 TKSITPBLKKNPCDDEPLCFENGVAHPRIDFANDKFTIGSEVWTYAND----VFKLGGEY 355
Oy 365 RPVDLTKTAACKLACKTN-----LEDASKY--PDLYEKDSVEVYCHDLVYVYTLVDVFG 416
Db 356 NPDFKFSKSLREFCNSMWTQILANSOKGYNSIPENFLKDA-----CFKGMVVLNIEHGFD 411
Oy 417 LDP-----EQEYTVANEIEYODALVEAMPYG 443
Db 412 MPRIDVDAENVDRPLQFSVEKEE-----RELSTWITG 444

```

RESULT 14

C86276
7A19.33 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C:Accession: C86276
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Comu, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hulcar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakono, H.
A:Authors: Rooney, T.; Rowley, D.; Sakono, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID: 21016719
A:Accession: C86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-508 <STO>
A:Cross-References: GB:AE005172; NID:95080800; PIDN:AA039310.1; GSPDB:GN00141
A:Genetics:
A:Map position: 1

Query Match 13.8%; Score 329; DB 2; Length 508;

Best Local Similarity 25.7%; Pred. No. 2.9e-16;

Matches 122; Conservative 88; Mismatches 179; Indels 86; Gaps 21;

```

Oy 4 TKAMDF-LISLMTFVFMPLPAISSOYLGNLIT--MNRKILLPKNOEPTVSVAVFADG 59
Db 29 TYSITIVIVACTIALGL-----FTGYSLIRSGRRKRVSL-----HTSVIIDG 73
Oy 60 STGSRYVYVNFQNDLLPLENELEFFYSVK--PGLSSYAANPEEAESLIPLLKEAENV 117
Db 74 SSOTRVHVGGRLESCKPVFDFGEENYASKLSPGLSAYADNEGSESTELVEPAKKR 133
Oy 118 VEPSQOPNTPVKLGATAGRLLEGNAENILQAVRDMLSKRSALNQSDAVSLDGTQEG 177
Db 134 VHKGLKSKDIRLMATAGKRLLELPVQEQILDVTRFVRS--SGFDRDMEASVISELLEN 192
Oy 178 SYLWVINTLLGKGRFTKTVGVNDLGGGVOMTYAASRNTPAKNPKVPEGSDPYIKKI 237
Db 193 FQDLMKV-YMLGIL-----LIMRSVRLLEVTV-----STELVP--SEFSRIL 231
Oy 238 VLQGRVYDLYVHSYLRGGEAPAEIIFKVAGSA-----NPCILAGF----- 279
Db 232 AYGNAVYNLYSHSFLDFGDDAQEKLESILYNSAANSTGEGVDPDCIPGIVLETNLQK 291
Oy 280 --DGATYGAEEKVAPASGSLUNCRKIALKAL-KVNAPCPYONCTPGGIMN---GGG 333
Db 292 DLPGLADKG-KFTATLQAAG-NFSECRSAAMLOEBKGGKTYKRCISIGSIFTPLNGS 349

```

```

Oy 334 GSGOKNLFTRSSPYLYSEDEVGIFVKNPKAIRPVDLTKTAACKLACKTNLEDASKYPDLYE 393
Db 350 FLATENEFHTSKFFGGEKEML-----SEMIILAGKRCGEGNSKIKAKYITTFPD 398
Oy 394 KDSVEVYCHDLVYVYTLVDVFG--LDPROEYTVANEIEYODALVEAMPPLGTAI 446
Db 399 ENILRR-CFSSAVIISMLHDSLGVALDD-ERIKYVASKAGEED--IPLDMALGAFI 449

```

RESULT 15

hypothetical protein T18B16.150 - Arabidopsis thaliana
T04439
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04439
R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Bancroft, I.; Mewes,
submitted to the Protein Sequence Database, April 1998
A:Reference number: 215359
A:Accession: T04439
A:Molecule type: DNA
A:Residues: 1-1052 <BEV>
A:Cross-References: EMBL:AL021687
A:Experimental source: cultivar Columbia; BAC clone T18B16
A:Genetics:
A:Map position: 4
A:Intons: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
A:Note: T18B16.150

Query Match 9.9%; Score 236.5; DB 2; Length 1052;

Best Local Similarity 22.6%; Pred. No. 5.1e-09;

Matches 108; Conservative 69; Mismatches 164; Indels 137; Gaps 20;

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Oy 54 VIFDAGSTGRVHY-----NFDONDLPLEVENL-----EYD--SVKPGSSRA 97
Db 525 LVYIVSITGTTRAVVOASINYYKDDSLPYMKSITFGISNRKGRAYDRMETEPGDKLV 584
Oy 98 ANPEEAESLIPLKEAENVVPSQOPNTPVKLGATAGRLLEGNAENILQAVRDMLSN 157
Db 585 NNRTGLTKAIKPLQWAEKOIPKNAHRTISLEYATAGVRRLRPADSSWILGNWSILA- 643
Oy 158 RSALNQSDAVSLDGTQEGSYLWVTIN--LLGRLGRFTKTVGVNDLGGGVOMTYA 214
Db 644 KSPFCRREWVKLIISGTEAEVFGWTALNYQTSMLGALPKK--ATFGALDGGSSLGVTFE 701
Oy 215 VSRNTAKNAPKVPPEGDPYIKLVLOGKKYDLYVHSYLRG-REAR----- 259
Db 702 NEERTHNETN-----LNLRIGSVNHHLASVLAGLNDARDRSVHLLKRLPNV 751
Oy 260 -RAEIKVAGGSANPCIIAGFDGAYVYSGAEVYVAPASG-----NLNOCRKI 307
Db 752 NKSDDLIEGLEKMKHPCLNSGNYOYICSOCASSVGGKKKSSVSTKLVGAPMNGEC--- 808
Oy 308 ALKALKVNAPC-----PYONCTPGGIMNGGSGOKNLFTRSSPYLYSEDEVGIFVKN 359
Db 809 --SALKKNAPCALPDGYPRH-----GQ-----FYANS--GEFV-- 838
Oy 360 PNAKIRPVDLTKTAACKLACKTNLEDASKYPDLYE-----DSVEYCHDLVYV 407
Db 839 -----VYREFNLSAESISLDDVLEKGRFEDKAMOVAKTSVSPQPIEQCFRAPYI 889
Oy 408 YTLVDGFGDPRQOEYTVANEIEYODALVEAMPPLGTAI---EATSS--LPKFERL 458
Db 890 VSLRGLYITDKQIITIGSGI-----TWTLGVALLESKALSLTGLKSYETL 938

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Search completed: June 28, 2002, 04:06:52

Job time: 376 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 02:12:41 ; Search time 19.5 Seconds
(without alignments)
578.699 Million cell updates/sec

Title: US-09-657-631-10

Perfect score: 2382

Sequence: 1 LHWTKAMDPLISLMTFVFM.....GTAIEALISLPKFERLMYFI 462

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Issued Patents-AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCYUS.COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/Backfill1est.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675.5	70.3	455	4	US-09-240-639-10 Sequence 10, Appl
2	1182.5	49.6	454	4	US-09-240-639-11 Sequence 11, Appl
3	491.5	20.6	428	4	US-09-608-285A-3 Sequence 3, Appl
4	491.5	20.6	428	4	US-09-608-285A-5 Sequence 5, Appl
5	491.5	20.6	428	4	US-09-240-639-6 Sequence 6, Appl
6	491.5	20.6	428	4	US-09-240-639-9 Sequence 9, Appl
7	486.5	20.4	428	4	US-09-608-285A-7 Sequence 7, Appl
8	472	19.8	405	4	US-09-608-285A-25 Sequence 25, Appl
9	463	19.4	484	4	US-09-240-639-2 Sequence 2, Appl
10	463	19.4	484	4	US-09-608-285A-27 Sequence 27, Appl
11	460	19.3	465	4	US-09-240-639-8 Sequence 8, Appl
12	443	18.6	473	4	US-09-240-639-12 Sequence 12, Appl
13	421.5	17.7	510	4	US-08-930-921-1 Sequence 1, Appl
14	392.5	16.5	471	4	US-09-608-285A-60 Sequence 60, Appl
15	315.5	13.2	529	4	US-09-240-639-4 Sequence 4, Appl
16	251.5	10.6	148	4	US-09-240-639-17 Sequence 17, Appl
17	224.5	9.4	154	4	US-09-240-639-14 Sequence 14, Appl
18	213	8.9	153	4	US-09-240-639-13 Sequence 13, Appl
19	197.5	8.3	153	4	US-09-240-639-15 Sequence 15, Appl
20	196	8.2	150	4	US-09-240-639-16 Sequence 16, Appl
21	106.5	4.5	1027	4	US-08-446-137B-2 Sequence 2, Appl
22	97	4.1	872	1	US-08-766-014-2 Sequence 2, Appl
23	95.5	4.0	905	4	US-09-074-658-70 Sequence 70, Appl
24	95	4.0	2004	1	US-08-375-709-15 Sequence 15, Appl
25	95	4.0	2004	1	US-08-752-929-15 Sequence 15, Appl
26	95	4.0	2004	4	US-09-090-793-9 Sequence 9, Appl
27	94	3.9	587	4	US-08-931-608A-4 Sequence 4, Appl

28	93	3.9	487	4	US-08-961-083-42 Sequence 42, Appl
29	92.5	3.9	761	4	US-09-625-188-14 Sequence 14, Appl
30	92	3.9	450	2	US-08-861-464-2 Sequence 2, Appl
31	92	3.9	450	2	US-08-396-001-2 Sequence 2, Appl
32	92	3.9	450	4	US-09-323-433A-2 Sequence 2, Appl
33	92	3.9	934	1	US-08-457-176-2 Sequence 2, Appl
34	92	3.9	934	1	US-08-457-175-2 Sequence 2, Appl
35	92	3.9	934	3	US-08-709-784-1 Sequence 1, Appl
36	92	3.9	934	4	US-09-651-658-3 Sequence 3, Appl
37	92	3.9	1112	2	US-08-714-402-2 Sequence 2, Appl
38	92	3.9	1161	4	US-09-327-536-2 Sequence 2, Appl
39	91	3.8	1403	2	US-08-387-942C-3 Sequence 3, Appl
40	88.5	3.7	2237	1	US-08-354-973-1 Sequence 1, Appl
41	88	3.7	564	3	US-08-425-843-8 Sequence 8, Appl
42	88	3.7	565	3	US-08-425-843-3 Sequence 3, Appl
43	87.5	3.7	1457	2	US-08-652-971-3 Sequence 3, Appl
44	87.5	3.7	1457	2	US-08-449-644-1 Sequence 1, Appl
45	87.5	3.7	1457	2	US-08-087-244A-1 Sequence 1, Appl

ALIGNMENTS

RESULT	1	US-09-240-639-10
Sequence 10, Application	US/09240639	
Patent No. 6350447		
GENERAL INFORMATION:		
APPLICANT: Chadwick, Brian Paul		
APPLICANT: Frischaut, Anna-Maria		
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE		
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS		
FILE REFERENCE: 9598-066		
CURRENT APPLICATION NUMBER: US/09/240,639		
CURRENT FILING DATE: 1998-01-29		
NUMBER OF SEQ ID NOS: 29		
SOFTWARE: PatentIn Ver. 2.0		
SEQ ID NO: 10		
LENGTH: 455		
TYPE: PRT		
ORGANISM: P. sativum		
US-09-240-639-10		
Query Match	70.3%	Score 1675.5; DB 4; Length 455;
Best Local Similarity	68.7%	Pred. No. 2.2e-165;
Matches 314; Conservative 64; Mismatches 76; Indels 3; Gaps 2;		
QY	7	MDPLISLMTFVFMPLMPAIISSOYLGNIIIMNRKILPKNOEPVTSYAVIFDAGSTGRVH 66
DB	1	MELLITLITFLFSPMPAITSSOYLGNLILTSKIFL--KOEIISYAVYFDAGSTGRH 58
QY	67	VYNFDNDILLPYENLEEFYDSVYKGLSSYANPEBAESLIPLKEANVPVVSQOPNT 126
DB	59	VYHFQNDLILHKGVEYEVYKKTPLSSYANPEQAKSLIPLBOARDVDDIQPKT 118
QY	127	PVKLGATAGLRLEGAENIIQAVYDMLSNSALWVQSDAYSILDQEGSLMTWTYV 186
DB	119	PVRLGATAGLRRLNGASEKILQSVYDMLSNSFTFVQDPAVSIIDQEGSLMTWTYV 178
QY	187	LGKLGKRTKTYGVVDLGGGSVQMTYAVSRNTAKNAPVEGEDPYIKKLYLGKKYD 246
DB	179	ALGNLCKKTKTYGVVDLGGGSVQMTYAVSRNTAKNAPVADDDPYIKKLYLGKIPYD 238
QY	247	VYHSYLRGREAIFRAEIFVAGGSANPCILAGFDGAYVYSGAEKYVSAPAGSMLNQCK 306
DB	239	YVHSYLFHFRASRAEILKTPRSPNCLLAGNGIYVSGEEFKATVATSGANFKCKN 298
QY	307	IALKAKVAPCPYQCTCGGIMNGGSGOKNLFITSSFYIYSEVQ--IFVAKPKAKIR 365
DB	299	TIRKAKLKYPCPYQCTCGGIMNGGSGOKNLFITSSFFYLPEDTGVAVDASTPFLIR 358
QY	366	PVDLKAATKACKTNLEDAKSKYPDLYEKDSVEYVCLDLYVYVTLVDGFGIDPFQEVTV 425

```
Db 359 PVDIETKAKACALNFEDAKSTYPLDKKNVASYCMLDIQYVLVDFGLDPLQKIT5 418
Qy 426 ANEITYOALVYEAAMPLGTATATATISLSEKFEPLAMFI 462
Db 419 GKIEYQDALVEAAMPLGNVAEIALPKEFLRMV 455
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```
RESULT 2
US-09-240-639-11
; Sequence 11, Application US/09240639
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; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 11
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-240-639-11
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```
Query Match 49.6%; Score 1182.5; DB 4; Length 454;
Best Local Similarity 51.1%; Pred. No. 3.8e-114;
Matches 226; Conservative 85; Mismatches 124; Indels 7; Gaps 4;
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Qy 11 ISLMTFVFMLEPAISSOYGCNNTIMNRKILPKNOEPVSYAVIFDAGSGSVHYXNF 70
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 9 IFILALFVPLSLSKNVAQPLRRLHLSHESEH---YAVIFDAGSGSVHYXNF 64
Qy 71 DONIDLLPVENELEFYDSVYKRGSLSSYANPEEAESLIPLIKEANVPVSOQPFPEVKL 130
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 65 DEKIGLPIGNNIEYFATERGLSSYAEPPKAANSLEPLDGEVGPQELQSEPLEL 124
Qy 131 GATGGLLEENAEENLQAVRDLNRSALNOSDAVSIIDTQOESYIMWTINYLK 190
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 125 GATGGLLEENAEENLQAVRDLNRSALNOSDAVSIIDTQOESYIMWTINYLK 190
Qy 191 LGRKFTYGVVDLGGGSVOMTYAVSHNTAKNAKVPEDGPYIKRLVLQKKYDLVYHS 250
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 185 LGRKYKSTTATIDGGGSVOMAYAINSEQFAKAPQNEDEG-PIYQOKHLSKDYINLYHS 243
Qy 251 YLRKGRAPFAEYFKVAGGSANPCITLAFPGAYTYSGAERYKVASPASGSLNOCRIALK 310
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 244 YLNGQLAGRAEYFKASRNSNPCALEGCGYYSYGVDYKVAKKSSMKRCRLRTRH 303
Qy 311 ALKNAPCPYONCTFGGIMWGGGSGOKNLFITSEFYLLSEDDGIFVKN-PNAKIRPVLD 369
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 304 ALKINACNIECTFNCGVWNGGGGOKNHASFFYDICAQVYIDTKFPPSLAPRIY 363
Qy 370 KTAAKLACKTNLEDAKSKYDLYEKDSVEYVCDLYVYVTLVLDGFGIDPFQCVYANET 429
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 364 LNAKAVACQTNVADIKSIFPKTQDR-NIPYLCMDLITYEYLLVDGGLNHRKBITYIHDV 422
Qy 430 EYODALVEAAMPLGTATATIS 451
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 423 QYKNYLVGAAMPLGCAIDLVSS 444
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```
RESULT 3
US-09-608-285A-3
; Sequence 3, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
```

```
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-3
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Query Match 20.6%; Score 491.5; DB 4; Length 428;
Best Local Similarity 31.3%; Pred. No. 2.3e-42;
Matches 134; Conservative 71; Mismatches 166; Indels 57; Gaps 14;
```

```
Qy 41 LIPKNOEPTSYAVITDASTGSRVHYVPDONL-DLPEVNELEFYDSVYKRGSLSSYAN 99
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 38 MCPINVASSTLVGIMPDASTGTRIHVYFVQKMPQOLPI-LEGFEVDSVKKGLSAFVQ 96
Qy 100 PEBAASLIPLIKEANVPVSOQPFPEVKLGTAGLRLEENAEENLQAVRDLNRS 159
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 97 PKGAFETVGLLEVAKDSIPRSHMKTPYVLKATAGRLRLEPKAKALLEVEKEIF-RKS 155
Qy 160 ALNVOSDAVSIIDTQOESYIMWTINYLKLGKRFKTVGVVDLGGGSVOMTYAVSRNT 219
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 156 PFLVPRKGSVSIIMDSDEGILAVTVFNLGQLHGRHOETVGTLDGASTQITFL-PQF 213
Qy 220 ANKAPRVPEGEDEPYIKKLVLQKKYDLVYHSYLRKGRFAF-----AEIKV 266
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 214 EYLEDTEPRG---YLTSEFMENSTYKLYTHSYLGLKAKARATLGALETGTDGHTFRS 270
Qy 267 AGGSANPCITLAFDADATYTSGAERYKVASPASGS-NLNOCRKIALKLVNAPCPYONCTF 325
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 271 A-----CLPRLMLEMWEIGVYKQYGGNGQBEVGEPEPCYAVLVAVNGKLLHQPE---- 320
Qy 326 GGIWNGGGSGGKNLFLISSFTY-LSEDDYGVFNKPNKIRPVLDLKTAKLACKTNLEDA 384
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 321 -----VORGSEFYAFSYYYDRAVDTDMIDYERKGLKVEDFERKAREVC-DNLENF 369
Qy 385 KSKYPDLYEKDSVEYVCDLYVYVTLVLDGFGIDPFQCVYANETLEYODALVEAAMPLGT 444
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 370 TSGSP-----FLCDDLSTYIALKDFG--FAUSTVL-QLTKRNNINETGVALGA 416
Qy 445 ATEAISTL 452
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 417 TFFHLOSL 424
```

```
RESULT 4
```


US-09-608-285A-7
 Sequence 7, Application US/09608285A
 Patent No. 6335013
 GENERAL INFORMATION:
 APPLICANT: Ford, John
 APPLICANT: Mulero, Julio
 APPLICANT: Yeung, George
 TITLE OF INVENTION: METHODS AND MATERIALS
 TITLE OF INVENTION: POLYPEPTIDES
 FILE REFERENCE: 28110/36570
 CURRENT APPLICATION NUMBER: US/09/608,285A
 CURRENT FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: 09/583,231
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 09/557,800
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/481,238
 PRIOR FILING DATE: 2000-01-11
 PRIOR APPLICATION NUMBER: 09/370,265
 PRIOR FILING DATE: 1999-08-09
 PRIOR APPLICATION NUMBER: PCR/US99/16180
 PRIOR FILING DATE: 1999-07-16
 PRIOR APPLICATION NUMBER: 09/350,836
 PRIOR FILING DATE: 1999-07-09

RESULT 8
 US-09-608-285A-25
 : Sequence 25, Application US/09608285A
 : Patent No. 6335013
 :
 : GENERAL INFORMATION:
 : APPLICANT: Ford, John
 : APPLICANT: Mulero, Julio
 : APPLICANT: Yeung, George
 : TITLE OF INVENTION: METHODS AND MATERIALS
 : TITLE OF INVENTION: POLYPEPTIDES
 : FILE REFERENCE: 28110/36570
 :
 : CURRENT APPLICATION NUMBER: US/09/608,285A
 :
 : CURRENT FILING DATE: 2000-06-30
 :
 : PRIOR APPLICATION NUMBER: 09/583,231
 : PRIOR FILING DATE: 2000-05-26
 :
 : PRIOR APPLICATION NUMBER: 09/557,800
 : PRIOR FILING DATE: 2000-04-25
 :
 : PRIOR APPLICATION NUMBER: 09/481,238
 : PRIOR FILING DATE: 2000-01-11

Query Match	19.8%;	Score 472;	DB 4;	Length 405;
Best Local Similarity	31.9%;	Pred. No. 2.2e-40;		
Matches 128; Conservative	66;	Mismatches 151;	Indels 56;	Gaps 13

RESULT 9
US-09-240-639-2

ORGANISM: Homo sapiens
US-09-240-639-2

Query Match	19.4%;	Score 463;	DB 4;	Length 456;
Best Local Similarity	31.3%;	Pred. No. 2.4e-39;		
Matches 131;	Conservative 70;	Mismatches 156;	Indels 62;	Gaps 13

RESULT 10

US-09-608-285A-27
; Sequence 27, Application US/09608285A

; Patent NO. 6335013
; GENERAL INFORMATION:

APPLICANT: Ford, John

APPLICANT: Muletto, Julie

APPLICANT: Ieung, George

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 28110/36570

CURRENT APPLICATION NUMBER: US/09/608,285A

; CURRENT FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: 09/583,231

PRIOR APPLICATION NUMBER: 09/557 800

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/481,238

PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: 09/370,265

PRIOR FILING DATE: 1999-08-09

PRIOR APPLICATION NUMBER: PCT/US99/1000 07 15

PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350 836

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/273,447

PRIOR FILING DATE: 1999-03-19

PRIOR APPLICATION NUMBER: 09/244,444

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: 09/122,443

PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/718 305

PRIOR FILING DATE: 1998-07-16

NUMBER OF SEO ID NOS: 60

```

; SOFTWARE: PatentIn Ver. 2.0

```

; SEQ ID NO 27

LENGTH: 484
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-608-285A-27

Query Match 19.4%; Score 463; DB 4; Length 484;
 Best Local Similarity 31.3%; Pred. No. 2,6e-39;
 Matches 131; Conservative 70; Mismatches 156; Indels 62; Gaps 13;

QY 52 YAVIFDAGSGSRVHYVNFQNDLLEFVNELEFYDSVKGLSSYAANPEBAESLIPLL 111
 DB 102 YGIMFDAGSGTRVHYVNFQNPREFPTLTH-ETFKAVKPGLSAYADDERKSAAGIRELL 160
 QY 112 KEENAVVPSQOPPTPKLATAGLRLLLEGNAENIIQAVRDMLSNKSALNVQDAVSTL 171
 DB 161 DVAKODIPFPFKATPVLVATATAGLRLLPEKAKKLOKKEVF-KASPELVGDVCVIM 219
 QY 172 DGTQEGSYLWVTINYLGLGKRFKTVGVVDLGGGSVQMTYAVSRNTAKNAPKV----- 226
 DB 220 NGTDEGSAMITINFLGSLKTPGSSVGMIDLGGSGTQIAF-----LPRVEGTIQ 270
 QY 227 --PEGEDPYIKKLVLOGKKDYVHSYLRGREAFAEIFKVAAGS-----ANPCIL 276
 DB 271 ASPPG--VLTALRMFRTYKLYSYSLGLMSARLAILGVGEGPAKDKKELVSPCLS 327
 QY 277 AGPDGATVSGAEKVSAPASGSLNQ-CRKIKAL--KVNAFCPYQNCPTFGGINNGG 333
 DB 328 PSFGEWEHEVETRVSGOKAASLHELCAARSEVLQNRHTEEVKHDF----- 379
 QY 334 GSGQKNLFLTSFYIASEDVGIFVKNPKNAPVYDLTAACKLACKTNLEDAKSKRPDLYE 393
 DB 380 -----YASYYDLAAGVGLDAEKGSVLVGDDEFIAKVCYRT-LEHQPOSSP----- 427
 QY 394 KDSVEYVCLDLYVYTLVDFGIDPQOEYTVANEITYODALVPAANPLGTAIAISL 452
 DB 428 ----FSCMDLTV-SLLLOEFGFPRSKVLKTRKIDN----VETSWALGAIHFYIDSL 476

RESULT 11
 US-09-240-639-8
 ; Sequence 8, Application US/09240639
 ; Patent No. 6350447
 ; GENERAL INFORMATION:
 ; APPLICANT: Chadwick, Brian Paul
 ; APPLICANT: Frischauf, Anna-Maria
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
 ; FILE REFERENCE: 9598-066
 ; CURRENT APPLICATION NUMBER: US/09/240,639
 ; CURRENT FILING DATE: 1998-01-29
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 465
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-240-639-8

Query Match 19.3%; Score 460; DB 4; Length 465;
 Best Local Similarity 30.1%; Pred. No. 5e-39;
 Matches 132; Conservative 68; Mismatches 174; Indels 64; Gaps 14;

QY 17 VFMLMPAIISSOYLGNINLRK-----LILPKNOEPTVSYAVIFDAGSGSRVH 66
 DB 8 VFMLIIAC-----VGSIVFYREQQTWEVGLSMCPINVSAGTFYGIIMFDAGSGTARIH 62
 QY 67 VYVNFQ-----NLDLLEPVNELEFYDSVKPGLSSYAANPEBAESLIPLLKEAVNVVVSQ 122
 DB 63 VYFVFOKTAQOLPFL-----EGEIFDSVKPGLSAIVDQPKQGAETVQVQELLEAVKKSIPRSH 118
 QY 123 QPMTPVKLGATAGLRLLLEGNAENIIQAVRDMLSNKSALNVQDAVSTLIDOTQGSYIHW 182

DB 119 WERTPVVLTATAGLRLLPEQKAQALLLEVEIEFKN-SPLVPODSVIMSGSEGLIAW 177
 QY 183 TINTLGLCKRFTKYGVVDLGGGSVQMTYAVSRNTAKNAPVBEEDPYIKKLVLOGK 242
 DB 178 TYNELTGQLHGRQEGTGTDLGASVQITFL--POREKTLQGPTRG--YLSFSEFENS 232
 QY 243 KYDLYVHSYLRGREAFAEIFKV--AGGS-----ANPCILAGPDGATVSGAEKVSAP 295
 DB 233 TFKLITHTSYLGFGLKARLALTLGALKEKTDGHTFRSACLPRLLEAEIMRGVKKYQCGN 292
 QY 296 ASGS-NINQCRKIALKAL--KVNAFCPYQNCPTFGGINNGGSGQKNLFLTSFYIASED 352
 DB 293 QEGEMGEPCYAEVLRYVQCKLHQPEEVRGSAF-----YAFSYYYDRAD 337
 QY 353 VGIIVNKNPKIRVYDLTAACKLACKTNLEDAKSKRPDLYEKDSVEYVCLDLYVYTLV 412
 DB 338 THLIDYEKGVALKVEDERRAREVC-DNLGSSSGS-----FLCMLITIALLK 387
 QY 413 DGFGLDPFOEYTVANEIE 430
 DB 388 DGLGFAERHPLTAHKESE 405

RESULT 12
 US-09-240-639-12
 ; Sequence 12, Application US/09240639
 ; Patent No. 6350447
 ; GENERAL INFORMATION:
 ; APPLICANT: Chadwick, Brian Paul
 ; APPLICANT: Frischauf, Anna-Maria
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
 ; FILE REFERENCE: 9598-066
 ; CURRENT APPLICATION NUMBER: US/09/240,639
 ; CURRENT FILING DATE: 1998-01-29
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 473
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 US-09-240-639-12

Query Match 18.6%; Score 443; DB 4; Length 473;
 Best Local Similarity 31.7%; Pred. No. 3e-37;
 Matches 142; Conservative 62; Mismatches 164; Indels 80; Gaps 16;

QY 52 YAVIFDAGSGSRVHYVNFQ-----ONLDDLPEVNELEFYDSVKPGLSSYAANPEBAE 105
 DB 48 YVIMIDAGSGSRVHYIKKFDVCTSPILLD-----EKFDMLPEPLSFDIDSVGAAN 99
 QY 106 SLIPLLKEAVNVVPSQOPPTPKLATAGLRLLLEGNAENIIQAVRDMLSNKSALN-VQ 164
 DB 100 SLIDPLLVANVYPIKARSCPVAVKATAGLRLLGDAKSSKILSAVBHDLEKDPFVYE 159
 QY 165 SDAYSILDTQEGSYLWVTINYLGLGKRFK--TYGVVDLGGGSVQMTYAVSRNTAKN 222
 DB 160 GDGVSIMGDEGEVFAWITNLYLGNIGANGPKLPTAIVDFLGGGSTOI--VEEPFPI 216
 QY 223 APKVPBEEDPYIKKLVLOGKKDYVHSYLRGREAFAEIFKVAAGSA----- 271
 DB 217 NEKAVDEHKF--DLKGDENYTLIYQSHLGTGLKEGRKNVSVLYVNAIKDKLIKCN 274
 QY 272 -----NPCI-----LAGPDGATVSGAEKVSAPASGSLNQCRKIALKALVNA 316
 DB 275 KTHCLSSPCLPKVNATNEKVTLESKEYT-IDFIDPERSGA---QCRLIDELIINKDA 330
 QY 317 PCPYQNCPTFGGINNGGSGQKNLFLTSFYIASEDVGIFVKNPKNAPKV----- 367
 DB 331 QCSPPCSFNGV-----HQPISLVRT--FKESNDIYIFSYFYDRTRTBLGMDLSFTLN 380

```

OY 368 DLTKAAKTLACTTNEDAKSKP---PLYEDSDVEYCLDLYVYTLTVGFGDPRQEV 423
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 381 ELNDLARKYVCGE-ETMNSVSSGSLAGSLDELSHSCFLDLSFVSLHHTGYDIPLOREL 439
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 424 TVANETETQDALVEANPLGTAIAISA 451
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 440 RTGKKI-----ANKELGWCGLASPLLKA 463
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 13
US-08-930-921-1
: Sequence 1, Application US/08930921B
: Patent No. 6287837
: GENERAL INFORMATION:
: APPLICANT: BEAUDOIN, Adrien R.
: APPLICANT: SEVIGNY, Jean
: TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
: TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
: TITLE OF INVENTION: TECHNOLOGY
: FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
: CURRENT APPLICATION NUMBER: US/08/930,921B
: CURRENT FILING DATE: 1998-01-02
: EARLIER APPLICATION NUMBER: PCT/CA96/00223
: EARLIER FILING DATE: 1996-04-10
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 510
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Description of Unknown Organism: unknown
: US-08-930-921-1

```

Query Match	17.7%	Score 421.5;	DB 4;	Length 510;
Best Local Similarity	27.4%	Pred. No. 5.9e-35;		
Matches 126;	Conservative 73;	Mismatches 174;	Indels 87;	Gaps 19

US-09-608-285A-60
Sequence 60, Application US/09608285A
Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60
LENGTH: 471
TYPE: prt
ORGANISM: Homo sapiens
US-09-608-285A-60

```

Query Match          16.5%; Score 392.5; DB 4; Length 471;
Best Local Similarity 31.7%; Pred. No. 5.3e-32;
Matches 108; Conservative 59; Mismatches 127; Indels 47; Gaps 9;

QY 52 YAVIDAGSTGSRVAVYFEDQNLIDLPENELEFDPVSKPGLSYAAANEAEASTLPLL 111
   |:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 102 YGIMFDASTGTRHVAHFQETRRPRETPPLTH-ETFKAVKPGLSAADVDEKAAQIGRELL 160
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 112 KEAENVVAVPSQOPNTPVKLGATAGLRLEGNAAENILQAVRDLMSNRSALNVQSDAVTL 171
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 161 DVAKODIPFDEKATPLVATKATAGLRLLPGEAKOKLLOKKEVF-KASFLVGDDCDSIM 219
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 172 DGTQGSGLVWVINTLLKLGKRFRTKYGVVDVGGSVOMTAAVSNRTKNAKPV----- 226
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 220 NGTIDGVSAMTITNLTGSLKTPGSSVGMGLDGGSTQIAF-----LPRVBTQ 270
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 227 --PEEEDPYIKLVLOGRKRYDLYVSYSLRYGREAERAELEFKVAGS-----ANPCIL 276
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 271 ASPPG---YLRALRFNNTYKLYSYSLGIGLMSARLAILGGVEOPAKDKGEIVSPCLIS 327
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 277 AGFDGAYVYSGAEKRVASAPAGSNNQ-CRKIALKAL-KVNAPCPYONCTFGGIWNGG 333
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 328 PSFKEMEHAEVYTRVSGQKAASLHELCAARVSEVLRQVRHRETEVKHYDF----- 379
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 334 GSGQKNLEFLTSEFYLSDEYGFVKKPNAKIRPVDLKTAAP 374
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 380 -----YAFSTYYDLAAGVGLIDAEKGGSLVAVGGFEIAR 413
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 14

RESULT 15
US-09-240-639-4
; Sequence 4, Application US/09240639

```

? Patent NO 6350447
? GENERAL INFORMATION:
? APPLICANT: Chadwick, Brian Paul
? APPLICANT: Frischauf, Anna-Maria
? TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
? TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
? FILE REFERENCE: 9598-066
? CURRENT APPLICATION NUMBER: US/09/240,639
? CURRENT FILING DATE: 1998-01-29
? NUMBER OF SEQ. ID NOS: 29
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 4
? LENGTH: 529
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-240-639-4

```

Query Match	13.2%	Score 315.5	DB 4	Length 529
Best Local Similarity	23.7%	Pred. No. 6.6e-24		
Matches 117	Conservative 85	Mismatches 198	Indels 93	Gaps 22

```

0Y 10 ILSLTFEMLPPLASSOYLGNNTLMNRKILILKNOEPYTSVAVIDAGSTGRVYN 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 IIALVVLVLSIVLVSTIV-----IQHKQVLP---PGKTIIVDAGSRTTYVYQ 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 70 FDONIDLLPVENE-----LEFYDSVK-PGLSSYAANPEBAESLIPLKAEENPVVS 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 W-----PAEKENNTGVVQSOTFKCSYVSGSISSTGNPNPDVPRAFEECMQKVKYGPSH 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 122 OOPNTPVKLTAGTAGIRLL---EGNAENIILOAVBDMILSNBALVQSDAVS ILDGTQEGS 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 LHGSPFIHLGATAGRRLRLRLONETNAENVELSIOSYFKSQP---FDRGAQIISGDEGV 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 179 YLWATINYLCK-LGKRP-----TKTVGVVDLGGGVQYMTYAASRNATKANAPVPE 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 YGMITANYLMGNFLEKMLMHMWVPHRGVETTGALDLOGASQIOSIFVAGEKMDLNTSD--- 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 229 GEDPIKILVLOGKKYDLYVSYLRYGR-LAFRAEIRKVAQS-----ANPCLLAGFDG 281
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 -----IMOVSLYGVYTLTYHSFQCYGRNEAEKKFLAMLIONSTPTKMLHTNPPCYRYSI 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 282 AYVYS---GAEYKVSAPASGSNLMQ-----CRKIALKALVNAAPCPYONTCFG 326
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 SFTMGHVFDSLCTYDQPRESYNPMDVITTEBGTGSPDLCKEKNVVASIPFKACHQOETCSFD 356
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 327 GIWNGGSGGKKNLFLT--SSFTYLSBDVGLFVKPNKIRPVDLKTAKLACTGN---LE 382
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 357 GVIYQ-----PKIKGFVFAAGYFYTAASLNT-----SGSFSLDTFNSTWFGCSOMNSQLP 407
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 383 DAKSKYPDLYEKDEVEVYCLDLYVYVTLVLDGFGDLDFOEYVANELEYODALVEYA--AW 440
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 408 ILLPKFDEVYARS---YCFSANIYIHLFVNGY---KFTBETNP-QIHFKEKGNSSIAM 459
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 441 PLGRATREKISSLP 453
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 460 SLGMYLSLTJNOIP 472
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: June 28, 2002, 04:01:08
Job time: 6507 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2002, 02:11:25 ; Search time 49.6 Seconds
(without alignments)
1034.599 Million cell updates/sec

Title: US-09-657-631-10

Perfect score: 2382
Sequence: 1 LHWTKAMDFLISLMTFVFM.....GTAIEAISSLPKEERLWYFI 462

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_032802.*
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2363	99.2	496 20	AAW85686
2	1684	70.7	462 20	AAW85684
3	1676.5	70.4	455 22	AAW81952
4	1665.5	69.9	486 20	AAW85685
5	1412.5	59.3	467 20	AAW85687
6	684.5	28.7	243 21	AAW82051
7	618.5	26.0	217 21	AAW82052
8	529.5	22.2	461 22	ABB66213
9	529.5	22.2	464 22	ABB59611
10	491.5	20.6	428 21	AAV44849
11	491.5	20.6	428 22	AAW72238

12	491.5	20.6	428 22	AAW72243	Human CD39 like pr
13	486.5	20.4	428 22	AAV44850	Human CD39-L4 vari
14	486.5	20.4	428 22	AAW72240	Human CD39 like pr
15	472	19.8	405 21	AAV44851	Human CD39-L66 pro
16	472	19.8	405 22	AAW72239	Human CD39 like pr
17	463	19.4	484 22	AAW72241	Human CD39 like pr
18	456	19.1	456 22	AAW93929	Human polypeptide,
19	426	17.9	464 21	AAV70899	Protein encoded by
20	426	17.9	464 21	AAV70922	Human soluble CD39
21	424.5	17.8	474 21	AAV70900	Protein encoded by
22	424.5	17.8	474 21	AAV70923	Human soluble CD39
23	424.5	17.8	476 21	AAV70889	Protein encoded by
24	424.5	17.8	476 21	AAV70912	Human CD39-L4-2/3
25	423	17.8	473 21	AAV70901	Protein encoded by
26	423	17.8	473 21	AAV70924	Human soluble CD39
27	423	17.8	487 21	AAV70898	Protein encoded by
28	423	17.8	487 21	AAV70921	Human soluble CD39
29	421.5	17.7	439 22	AAW71918	Soluble human CD39
30	421.5	17.7	454 21	AAV70890	Protein encoded by
31	421.5	17.7	454 21	AAV70913	Human soluble CD39
32	421.5	17.7	463 21	AAV70902	Protein encoded by
33	421.5	17.7	463 21	AAV70925	Human soluble CD39
34	421.5	17.7	476 21	AAV70888	Protein encoded by
35	421.5	17.7	476 21	AAV70911	Human CD39-L4-1 pr
36	421.5	17.7	478 21	AAV70891	Protein encoded by
37	421.5	17.7	478 21	AAV70914	Human soluble CD39
38	421.5	17.7	510 17	AAW04264	Human CD39 protein
39	421.5	17.7	510 17	AAW04334	Human lymphoid cel
40	421.5	17.7	510 21	AAV70887	Human soluble CD39
41	421.5	17.7	510 21	AAV70910	Human soluble CD39
42	421.5	17.7	510 22	AAV71917	Human CD39. Homo
43	416	17.5	462 22	AAU30882	Novel human secret
44	392.5	16.5	471 22	AAW72242	Mature human CD39
45	361.5	15.2	495 20	AAV33296	Human membrane spa

ALIGNMENTS

RESULT 1	
AAW85686	standard; Protein; 496 AA.
XX	
AC	AAW85686;
XX	
DT	19-JUL-1999 (first entry)
XX	
DE	NBP46 root lectin.
XX	
KW	NBP46; lectin; Rhizobium; leguminous plant; transgenic plant;
KW	nitrogen; nitrogen fixation; fertilizer.
XX	
OS	Lotus japonica.
XX	
Key	Location/Qualifiers
FT	Misc-difference 234
FT	/note="this residue is encoded by nucleotides
FT	missing from the specification, and so
FT	cannot be identified"
FT	Misc-difference 252
FT	/note="this residue is encoded by nucleotides
FT	missing from the specification, and so
FT	cannot be identified"
FT	Misc-difference 270
FT	/note="this residue is encoded by nucleotides
FT	missing from the specification, and so
FT	cannot be identified"
PN	W09907223-A1.
XX	
PD	18-FEB-1999.
XX	
PF	05-AUG-1998; 98WO-US16261.

0

XX	19-JUL-1999	(first entry)	
DT			
XX			
DE	NBP46 root lectin.		
XX			
KW	NBP46; lectin; Rhizobium; leguminous plant; transgenic plant;		
RW	nitrogen; nitrogen fixation; fertilizer.		
XX			
OS	Dolichos biflorus.		
XX			
EH	Key	Location/Qualifiers	
FT	Region	52..73	
FT		/label= "Conserved_region	
FT		/note= "Conserved among various plant and animal	
FT	Region	apyrases"	
FT		128..144	
FT		/label= "Conserved_region	
FT		/note= "Conserved among various plant and animal	
FT		apyrases"	
FT	Modified-site	139	
FT		/note= "Potential N-glycosylation site"	
FT	Region	153..175	
FT		/label= "Conserved_region	
FT		/note= "Conserved among various plant and animal	
FT	Region	apyrases"	
FT		160..180	
FT		/label= "Conserved_region	
FT		/note= "Conserved among various plant and animal	
FT	Modified-site	276	
FT		/note= "Potential N-glycosylation site"	
XX			
XX	WC9907223-71.		
PN			
XX	18-FEB-1999.		
PD			
XX			
PF	05-AUG-1998;	98WO-US16261.	
XX			
PR	06-AUG-1997;	97US-0907226.	
XX			
XX	(REGC) UNIV CALIFORNIA.		
PA			
PI	Etzler ME, Murphy JB;		
DR	WPI, 1999-167136/14.		
DR	N-PSDB; AA08522.		
XX			
PT	New polynucleotides encoding Nod factor binding lectins - useful		
PT	for production of transgenic plants which are able to fix nitrogen		
PS	Claim 7; Page 43; 57pp; English.		
XX			
CC	The NBP46 root lectin is instrumental in recognising and binding		
CC	to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate		
CC	interaction. The production of transgenic plants comprising an		
CC	expression cassette expressing the NBP46 root lectin is advantageous		
CC	since it would mean that non-leguminous plants could fix nitrogen		
CC	from the atmosphere, lessening the need for the addition of nitrogen		
CC	containing fertilizer to soil. This would lead to higher crop yields		
CC	where soil has been overplanted and replenishment of the depleted		
CC	soil with usable nitrogen. Alternatively, expression of NBP46 can be		
CC	used to modulate oligosaccharide signalling in the plant. The nucleic		
CC	acid sequences can be used to inhibit expression of an endogenous		
CC	gene and also to suppress endogenous NBP46 gene expression.		
XX			
XQ	Sequence 462 AA;		

Db 1 mrvvwpktsmsfll-11tflfslpkissgyvgnsl1nhkklip-ngelltsyavif 58
QY 57 DAGSTSRHVHYVFDONDLPLPVENLEFDSYKPGLSSTAAANPEEAESLIPLEAEEN 116
Db 59 dagssgsrvhvfndqnl1l1hgnld1etkklpglssyadpekaaesl1p1leaead 118
QY 117 VVPSQOPMTVPVKLTAGTARLEEGNAENIIQAVRDMLSNRSALNVSQAVSILDTGTOE 176
Db 119 vvpelhpctplk1gataq1r1ldgdaek1l1qavremfrnssls1svqpaavsl1q1tqe 178
QY 177 GSYLWMTINYLGLGKLRFTKTVGVVDLGGSVQMTYAVSRNTAKNAPKVEGEDPYIKK 236
Db 179 gsy1w1t1v1y1l1g1k1g1t1e1k1t1e1t1v1d1g1s1v1q1m1a1y1s1r1n1t1a1k1n1a1p1k1v1e1g1e1d1p1y1i1k1 238
QY 237 LVLOGKKYLYVHSYLRGREGARAEIFKVAGGSANPCILAGFGAVTYSGAERYKSAPA 296
Db 239 lv1kgkkyd1y1h1s1y1l1r1g1n1d1a1r1v1k1f1k1t1d1g1a1s1p1c1l1a1g1e1d1y1r1y1s1g1e1s1y1n1y1p1t 298
QY 297 SGNLNOGCKRIALKALKVNAPOYONCTFGIWNNGGSGOKMLFTSSSFYLSDEVGTF 356
Db 299 sgantfecdl1a1q1l1r1l1e1p1e1s1h1e1n1c1t1g1w1d1g1g1k1s1g1q1k1n1l1v1t1s1a1l1y1r1s1e1v1g1-f 357
QY 357 VKNPNAKIRPVDLKTAALACTNLEDAKSKYPDLXEKDSVEYVCIDL1VYVTL1VDGFG 416
Db 358 v1r1p1n1a1k1r1p1v1d1l1k1t1a1l1a1c1t1n1l1e1d1a1k1s1k1y1p1d1l1x1e1k1d1s1v1e1y1c1i1d1l1v1y1t1l1v1d1g1f1g 416
QY 417 LDPQEVVYVANEIYODALVEAAMP1GTAIEA1SSLPKFER1MYFT 462
Db 417 ldp1e1g1e1t1v1a1e1g1e1y1g1d1a1v1e1t1a1p1g1t1a1e1a1s1s1p1k1f1e1r1m1y1f1 462

RESULT 3

AAB81952
ID AAB81952 standard; protein: 455 AA.
XX
AC AAB81952;
XX
DT 25-JUN-2001 (first entry)
XX
DE Pea blight resistance protein.
XX
KW Pea; blight resistance; nucleotide triphosphate decomposition.
XX
OS Pisum sativum.
XX
PN JP2001017176-A.
XX
PD 23-JAN-2001.
XX
PF 02-JUL-1999; 99JP-0189129.
XX
PR 02-JUL-1999; 99JP-0189129.
XX
PA (KYOU) UNIV KYOTO.
XX
DR MPI: 2001-320697/34.
DR N-PSDB; AAF85679, AAF85680, AAF85681.
XX
PT New blight-resistant polypeptide useful for giving blight resistance to
XX a plant -
XX
PS Claim 1: Page 12; 20pp; Japanese.
XX
CC The present invention provides the protein and coding sequences of a
XX pea protein with nucleotide triphosphate decomposing activity. The gene
XX can be used for conferring blight resistance on a plant. The present
XX sequence is the protein of the invention.
SQ Sequence 455 AA;

Query Match 70.4%; Score 1676.5; DB 22; Length 455;

Best Local Similarity 68.7%; Pred. No. 1,9e-146;
Matches 314; Conservative 64; Mismatches 76; Indels 3; Gaps 2;

QY 7 MDPLISLMTFVFMALRAISSQYLGNNIILNKRILLPKNOEPTSTAVITDAGSTGSRVH 66
Db 1 m1e1l1i1k1l1f1l1s1m1p1l1e1s1s1y1l1g1n1l1t1s1r1i1f1--k1e1e1s1y1a1v1d1a1g1s1t1s1r1h 58
QY 67 VVPSQOPMTVPVKLTAGTARLEEGNAENIIQAVRDMLSNRSALNVSQAVSILDTGTOE 126
Db 59 v1v1p1s1q1o1p1m1t1v1p1k1l1t1a1g1t1a1r1l1e1e1g1n1a1e1n1i1i1q1a1v1r1d1m1l1s1n1r1s1a1l1n1v1s1q1a1v1s1i1l1d1t1g1t1o1e1s1y1l1a1m1t1i1n1y 118
QY 127 PVKLGATAGLRLEEGNAENIIQAVRDMLSNRSALNVSQAVSILDTGTOE 186
Db 119 p1v1r1l1g1a1t1a1g1r1l1l1n1g1d1a1s1e1k1l1g1s1v1r1d1m1l1s1n1r1s1t1f1n1v1q1p1a1v1s1i1l1d1t1g1e1g1s1y1l1w1t1v1y 178
QY 187 LGLCKLRFTKTVGVVDLGGSVQMTYAVSRNTAKNAPKVEGEDPYIKKLV1LOGKKYDL 246
Db 179 l1g1l1k1l1r1f1t1k1t1v1g1v1d1l1g1g1s1v1q1m1a1y1a1v1s1k1t1a1k1n1a1p1k1v1e1g1e1d1p1y1i1k1k1v1l1k1p1y1d1 238
QY 247 VVHSYLRGREGARAEIFKVAGGSANPCILAGFGAVTYSGAERYKSAPASGNLNOGCKR 306
Db 239 v1v1h1s1y1l1r1g1r1e1a1r1a1e1i1f1k1v1a1g1s1a1n1p1c1i1l1a1g1f1n1g1y1l1y1s1g1r1i1k1a1t1a1y1s1g1a1n1f1n1c1k1n 298
QY 307 IALKALKVNAPOYONCTFGIWNNGGSGOKMLFTSSSFYLSDEVG-IFVKNPNAKIR 365
Db 299 t1r1k1a1l1k1l1n1y1p1c1y1n1c1t1f1g1w1n1g1g1n1g1q1k1l1f1a1s1s1f1y1p1e1d1t1g1m1d1a1s1t1p1n1f1l1r 358
QY 366 PVDLKTAAK1ACKTNLEDAKSKYPDLXEKDSVEYVCIDL1VYVTL1VDGFG1DLPQEVTV 425
Db 359 p1v1d1l1e1k1t1a1k1e1a1c1n1f1e1d1a1s1t1y1p1f1l1d1k1n1v1a1s1c1m1d1l1y1v1l1v1d1g1f1g1d1p1q1i1t1s 418
QY 426 ANE1YODALVEAAMP1GTAIEA1SSLPKFER1MYFT 462
Db 419 g1k1e1y1q1d1a1v1e1a1w1p1l1g1n1a1v1e1a1s1l1p1k1f1e1r1m1y1t1v 455

RESULT 4

AAM85685
ID AAM85685 standard; protein: 486 AA.
XX
AC AAM85685;
XX
DT 19-JUL-1999 (first entry)
XX
DE NBP46 root lectin.
XX
KW NBP46; lectin; Rhizobium; leguminous plant; transgenic plant;
XX nitrogen; nitrogen fixation; fertilizer.
XX
OS Medicago sativa.
XX
FH Key Location/Qualifiers
FT MISC-difference 460 /note- "Encoded by TAA stop codon"
FT MISC-difference 470 /note- "Encoded by TAA stop codon"
FT MISC-difference 479 /note- "Encoded by TAA stop codon"
XX
PN MO9907223-A1.
XX
PD 18-FEB-1999.
XX
PE 05-AUG-1998; 98WO-US16261.
XX
PR 06-AUG-1997; 97US-0907226.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Etzler ME, Murphy JB;
XX
DR MPI: 1999-167136/14.
DR N-PSDB; AAX08528.

4;

RESULT	5
AAW85687	
ID	AAW85687 standard; Protein; 467 AA.
XX	
AC	AAW85687;
XX	
DT	19-JUL-1999 (first entry)
XX	
DE	DBX oligosaccharide signalling protein.
XX	
KW	NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen; nitrogen fixation; fertilizer.
KW	
XX	
XX	Dolichos biflorus.

Query Match	59.3%;	Score 1412.5;	DB 20;	Length 467;
Best Local Similarity	59.4%;	Pred. No. 5.7e-122;		
Matches 278;	Conservative 68;	Mismatches 109;	Indels 13;	Gaps 5

[illegible]

Db 302 sgaefekcqnvvleaahvnatcsykdcftfgylwngggagennffvasiffevadeag-f 360
Qy 357 V--NRKNATIRPYDLKTAKTKLEDAKSKYPPDLYEKDSVEYCDLVYYTLLVNG 414
Db 361 vopndanaivrvpfdedaakvacaetelkalksvfprvkqgd-vpyicldlvgytllvqg 419
Qy 415 FGLDPQEQETVANEIEYODALVEAMPGLGTATFAISLSLPRKPERLMEFI 462
Db 420 fgldpqgetltlvrgldyqds]veaawplgsaleaalslpkfeklmlyfi 467
RESULT 6
ID AAG22051 standard: Protein; 243 AA.
AC AAG22051;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 24833.
DE Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX Arabidopsis thaliana.
OS
XX
PN EP1033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 990S-0121825.
PR 05-MAR-1999; 990S-0123180.
PR 09-MAR-1999; 990S-0123548.
PR 23-MAR-1999; 990S-0125788.
PR 25-MAR-1999; 990S-0126264.
PR 29-MAR-1999; 990S-0126785.
PR 01-APR-1999; 990S-0127462.
PR 06-APR-1999; 990S-0128234.
PR 08-APR-1999; 990S-0128714.
PR 16-APR-1999; 990S-0129845.
PR 19-APR-1999; 990S-0130077.
PR 21-APR-1999; 990S-0130449.
PR 23-APR-1999; 990S-0130510.
PR 23-APR-1999; 990S-0130891.
PR 28-APR-1999; 990S-0131449.
PR 30-APR-1999; 990S-0132048.
PR 30-APR-1999; 990S-0132407.
PR 04-MAY-1999; 990S-0132484.
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PR 29-JUN-1999; 990S-0140991.
PR 30-JUN-1999; 990S-0141287.
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PR 01-JUL-1999; 990S-0142154.
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PR 06-JUL-1999; 990S-0142390.
PR 08-JUL-1999; 990S-0142803.
PR 09-JUL-1999; 990S-0142920.
PR 12-JUL-1999; 990S-0142977.
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PR 15-JUL-1999; 990S-0144005.
PR 16-JUL-1999; 990S-0144085.
PR 16-JUL-1999; 990S-0144086.
PR 19-JUL-1999; 990S-0144325.
PR 19-JUL-1999; 990S-0144331.
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PR 20-JUL-1999; 990S-0144352.
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PR 20-JUL-1999; 990S-0144884.
PR 21-JUL-1999; 990S-0144814.
PR 21-JUL-1999; 990S-0145086.
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PR 22-JUL-1999; 990S-0145088.
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PR 26-JUL-1999; 990S-0145276.
PR 27-JUL-1999; 990S-0145913.
PR 27-JUL-1999; 990S-0145918.
PR 27-JUL-1999; 990S-0145919.
PR 28-JUL-1999; 990S-0145951.
PR 02-AUG-1999; 990S-0146386.
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PR 04-AUG-1999; 990S-0147204.
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PR 06-AUG-1999; 990S-0147303.
PR 06-AUG-1999; 990S-0147416.
PR 09-AUG-1999; 990S-0147493.

PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
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PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
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PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 13-OCT-1999; 99US-0159294.
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PR 18-OCT-1999; 99US-0159584.
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PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
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Query Match 28.7%; Score 684.5; DB 21; Length 243;
Best Local Similarity 52.9%; Pred. No. 5.7e-55;
Matches 129; Conservative 46; Mismatches 64; Indels 5; Gaps 4;
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QY 211 ANPCLAGFDGATYVYSGAEYVSA PASGSNINOCRKIALAKLV-NAPCPYONCTFGGIW 329
Db 61 nmpclatgyagtlkyggkafkaaspsgasidccrrvalnalkvmslchmctfsgvw 120
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QY 388 YPDLYEKDSVEYVCLDIIVYVTLVDFGGLDPFOEYVANEIEYODALVPAAMP|GTAIE 447
Db 180 fprv-eednlpylclldlvyyqtl|lvdgfg|kpsqtl|lvkvvgygdyaavaaplgsaie 238
QY 448 AISS 451
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ID AAG22052 standard; Protein; 217 AA.
XX
AC AAG22052;
XX
DE 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24834.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EF1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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PR 08-APR-1999; 99US-0128714.
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PR	28-OCT-1999	9905-0161920


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Db      156 pflvpgsvsindgsdeglawtvtntflcgqlhgrhgtvvgldlpgastqtlfl- -pgf 213
QY      220 AKNAAPVPEGEDEPYIKKLVLOGKKYDLVYHSYLRYGREAFR-----AEIRKV 266
Db      214 ektleqtprg---yltsfemfnsytklyhsylgfglkaarlalgaletegtdhtfrs 270
QY      267 AGGSANPCILAGFDGAVTYTSGAEKVSAPASGS-NLNOCRKIALAKLVNAPCPYONCTF 325
Db      271 a-----clprvlaeawifgvkygvgngqgevegfepeyaevlrvvgkllhqpae--- 320
QY      326 GGIMWNGGGSGQKNLFLTSSFYI-LSEVYGIFVNNKPNKIRPVDLKTAAKLTAKTNLEDA 384
Db      321 -----vqrgsfyafsytydravtdmdldyegkglkvedferkarevc-dnlenf 369
QY      385 KSKYPDLVEKDSVEYVCLDIYVYVTLVDGRLDPFOEVTYVANEIEYDAILVEAAMPVGT 444
Db      370 tsgsp-----flcmdlsyitalikdfig---fadstvl-qltkkvnmetgwaiga 416
QY      445 AIEAISL 452
Db      417 tfhlqsl 424

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RESULT 11

AAB72238 ID AAB72238 standard; Protein: 428 AA.

AC AAB72238;

DT 14-MAY-2001 (first entry)

DE Human CD39 like protein CD39-L4 amino acid sequence.

XX Human CD39-like protein; apyrase; NDpase; platelet function inhibitor;

KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;

KM cerebral artery thrombosis; platelet aggregation; inflammation;

KW apoptosis; autoimmune disorder; neurological disorder;

KM Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.

OS Homo sapiens.

XX Wo200110205-A1.

XX 15-FEB-2001.

PF 09-AUG-2000; 2000WO-US21790.

XX 09-AUG-1999; 99US-0370265.

PR 11-JAN-2000; 2000US-0481238.

PR 25-APR-2000; 2000US-0557800.

PR 26-MAY-2000; 2000US-0583231.

PR 30-JUN-2000; 2000US-0608285.

XX (HYSE-) HYSEQ INC.

PI Ford J, Mulero JT, Yeung G;

XX WPI, 2001-147489/15.

DR N-PSDB; AAF63383.

XX Polynucleotides encoding human CD39-like polypeptides, with apyrase

PT and/or NDpase activity, which are useful in the treatment of

PT pathological conditions caused by thrombosis (e.g. myocardial

PT infarction) and inflammatory disorders -

```

CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NDps. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
CC cytokine overstimulation), autoimmune disorders such as thrombosis,
CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
CC neurological disorders including neurodegenerative diseases, epilepsy,
CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, and amyotrophic lateral sclerosis; and cancer. The present
CC sequence represents human CD39 like protein CD39-L4.
XX
SQ Sequence 428 AA;

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Query Match 20.6%; Score 491.5; DB 22; Length 428;

Best Local Similarity 31.3%; Pred. No. 1e-36;

Matches 134; Conservative 71; Mismatches 166; Indels 57; Gaps 14;

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QY 41 LLEKNOEPTSYAVIPDAGSTGRVHYNFDQNL-DLPEVNELEFYDSVKGQLSSYAAN 99
Db      38 mcpinvasatlyimfdastgrlhytftvgkmpgqlpl-legevfdsvkpglsafvdq 96
QY 100 PEEAESTLIPLEKAEVNVVVSQQPNTPVKLGATAGLRILEGNAANIIQANVDMLSNRS 159
Db      97 pkqgaetvqgllevakdsiprshkktvplvkataglrllpekkakallfevkeft-rxs 155
QY 160 ALNVQSDAVSIIDTQEGSYLWNTINYLKLEKRTKTVGVVDLGGSSVQMTYAVSRMT 219
Db      156 pflvpgsvsindgsdeglawtvtntflcgqlhgrhgtvvgldlpgastqtlfl- -pgf 213
QY 220 AKNAAPVPEGEDEPYIKKLVLOGKKYDLVYHSYLRYGREAFR-----AEIRKV 266
Db      214 ektleqtprg---yltsfemfnsytklyhsylgfglkaarlalgaletegtdhtfrs 270
QY 267 AGGSANPCILAGFDGAVTYTSGAEKVSAPASGS-NLNOCRKIALAKLVNAPCPYONCTF 325
Db      271 a-----clprvlaeawifgvkygvgngqgevegfepeyaevlrvvgkllhqpae--- 320
QY 326 GGIMWNGGGSGQKNLFLTSSFYI-LSEVYGIFVNNKPNKIRPVDLKTAAKLTAKTNLEDA 384
Db      321 -----vqrgsfyafsytydravtdmdldyegkglkvedferkarevc-dnlenf 369
QY 385 KSKYPDLVEKDSVEYVCLDIYVYVTLVDGRLDPFOEVTYVANEIEYDAILVEAAMPVGT 444
Db      370 tsgsp-----flcmdlsyitalikdfig---fadstvl-qltkkvnmetgwaiga 416
QY 445 AIEAISL 452
Db      417 tfhlqsl 424

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RESULT 12

AAB72243 ID AAB72243 standard; Protein: 428 AA.

AC AAB72243;

DT 14-MAY-2001 (first entry)

DE Human CD39 like protein CD39-L4 amino acid sequence.

XX Human CD39-like protein; apyrase; NDpase; platelet function inhibitor;

KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;

KM cerebral artery thrombosis; platelet aggregation; inflammation;

KW apoptosis; autoimmune disorder; neurological disorder;

KM Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.

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Oy 41 LLPKNOEPTSYAIVIPAGSNGSVHNYNPONL-DLLPENENLEFDPYSPGGLSSAAN 99
Db 38 mcpnlvsaastlygmfaagsvgtrlnhytltvqkmpgqpl-legevtdsvkpgjalsatvdq 96
Oy 100 PEEAAESTLIPLLKEAENVVPVSOOPNTPVKLGATVAGRLLEGNAENILLOAVRDLMSNRS 159
Db 97 pkgaetevqgllevakdsipshvkktepvvllkacagtrilipenbakallfevfev-rks 155
Oy 160 ALNOSDPAVSLIDSGOESSYLMWTINYLTLGKRRFTKTVGVNDLGGSSVOMPRYASRNT 219
Db 156 pflvpkgsvtlmogsdogllawtvlvnlftqglhngretvgtldlgasqgltfi--pqf 213
Oy 220 AKNAAPVEGEDPYIKKLVLQGGKKYDLYVHSYLYRGAEAF-----AETIKV 266

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as ACR III mutant protein, an apyrase and/or nucleotide diphosphatase

QY 326 GGIWNGGSGGOKNLFUTSSFY-LSEYGVFNKRNKIRPVDLTKAKTNLEDA 384
 Db 321 -----vgrsfyatsyydravtdcmidyekgylkvedferkarevc-dnlentf 369
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 QY 445 AIEAIISSL 452
 Db 417 tflhlqsl 424

RESULT 15
 AAY44851
 ID AAY44851 standard; Protein; 405 AA.
 AC AAY44851;
 XX
 DT 18-MAY-2000 (first entry)
 XX
 DE Human CD39-L66 protein.
 XX
 KM CD39-L4; human; CD39-L66; apyrase; nucleotide diphosphatase; NDPase;
 KM ATP diphosphohydrolase; ATPdase; adenosine diphosphate; ADP; treatment;
 KM platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
 KM cerebral ischemia; angina; vascular graft; extracorporeal circulation;
 KM molecular weight marker; nutritional supplement; tumour; prevention;
 KM drug targeting; splice variant.
 OS Homo sapiens.
 XX
 PN WO200004041-A2.
 XX
 PD 27-JAN-2000.
 XX
 PF 16-JUL-1999; 99WO-US16180.
 XX
 PR 16-JUL-1998; 98US-0118205.
 PR 24-JUL-1998; 98US-0122449.
 PR 04-FEB-1999; 99US-0244444.
 PR 19-MAR-1999; 99US-0273447.
 PR 09-JUL-1999; 99US-0350836.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Ford J, Mulero J;
 XX
 DR WPI: 2000-182397/16.
 DR N-PSDB: AAZ50358.
 XX
 PT New nucleic acid encoding human CD39-Like protein, useful for treating
 PT and preventing thrombotic disease -
 XX
 PS Claim 15; Page 124-125; 125pp; English.
 XX
 CC The present amino acid sequence is the CD39-L66 protein, a splice
 CC variant of the CD39-L4 protein. It is an apyrase and/or nucleotide
 CC diphosphatase (NDPase), isolated from the human foetal liver-spleen cDNA
 CC library, b2HFLS20W. It is a soluble ATP diphosphohydrolases (ATPdase) and
 CC is involved in the hydrolysis of adenosine diphosphate (ADP), the agonist
 CC that causes platelet aggregation. CD39-L4 protein has 308 and 808
 CC homology to human and murine CD39. It has platelet aggregation inhibition
 CC and antithrombotic activity. CD39-L4 is used to treat or prevent
 CC thrombosis, myocardial infarction, cerebral ischemia and angina. It is
 CC also used in vitro, to maintain vascular grafts or during extracorporeal
 CC circulation, to hydrolyse NDP, as molecular weight markers and as
 CC nutritional supplements. It is used to identify therapeutic agents that
 CC bind and modulate CD39-L4. It is coupled to toxins for targeting drugs
 CC to tumours or other cells that express CD39-L4.
 XX
 SQ Sequence 405 AA;

Query Match 19.8%; Score 472; DB 21; Length 405;
 Best Local Similarity 31.9%; Pred. No. 5,9e-35;
 Matches 128; Conservative 66; Mismatches 151; Indels 56; Gaps 13;

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 QY 100 PEEAESLIPLIKEAENVVPSOOPNTPVKLGATAGLRILEGNAENIIOAVRDMISNR 159
 Db 97 pkgaetvqgllevakdsiprshwkktpvlikatagrlilpenhkaallfevkelf-rks 155
 QY 160 ALNVOGDASIIDGTOEGSYLWTTIYLLGKLGKRTKTGVGVDDGGGVSOMTYANSRNT 219
 Db 156 pflvpkgsvsindgsdeglawvtnfltcqqlhghrqtvgctldlggastqltfl--pgf 213
 QY 220 AKNAPKVPEDGEPYIKKLVLOGKKYDLYVHSYLRVGREAFR-----AEIFRV 266
 Db 214 ektlqetprg---yltsfemfnstkyklyhsylgfglkaariatlgaletgtdhtfrs 270
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 QY 326 GGIWNGGSGGOKNLFUTSSFY-LSEYGVFNKRNKIRPVDLTKAKTNLEDA 384
 Db 321 -----vgrsfyatsyydravtdcmidyekgylkvedferkarevc-dnlentf 369
 QY 385 KSKYPDLYEKDSVEYVCLDLVYVYTLVDGFGIDPFOEYTV 425
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 Job time: 6549 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 03:52:41 ; Search time 19.6 Seconds

(without alignments)
912.675 Million cell updates/sec

Title: US-09-657-631-10

Perfect score: 2382

Sequence: 1 LHWTKAMDFLISLMTFVEML.....GTAIEAIISSLPKFERLMYFI 462

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1182.5	49.6	454	1 APY_SOLTU	P80595 Solanum tub
3	491.5	20.6	428	1 ENP5_HUMAN	O75356 homo sapien
4	479	20.1	427	1 ENP5_MOUSE	O9wuz9 mus musculu
5	468	19.6	469	1 ENP5_MESAU	O9yvc8 mesocricetu
6	463	19.4	484	1 ENP6_HUMAN	O73554 homo sapien
7	453.5	19.0	435	1 ENP6_RAT	O9er31 rattus norv
8	442.5	18.6	518	1 GDA1_YEAST	P37621 saccharomyc
9	424	17.8	511	1 ENP1_RAT	P97687 rattus norv
10	421.5	17.7	510	1 ENP1_HUMAN	P49961 homo sapien
11	410.5	17.2	510	1 ENP1_MOUSE	P55772 mus musculu
12	406	17.0	513	1 ENP1_BOVIN	O18956 bos taurus
13	398.5	16.7	494	1 ENP2_CHICK	O21815 caenorhabdi
14	378.5	15.9	557	1 YB04_CAEEL	O21815 caenorhabdi
15	378	15.9	495	1 ENP2_RAT	O35795 rattus norv
16	375	15.7	485	1 YV4E_CAEEL	O18411 caenorhabdi
17	372	15.6	493	1 ENP1_CHICK	O93295 gallus galli
18	369.5	15.5	510	1 ENP1_PIG	O9myu4 sus scrofa
19	368.5	15.5	495	1 ENP2_HUMAN	O9y513 homo sapien
20	358	15.0	495	1 ENP2_MOUSE	O55026 mus musculu
21	343.5	14.4	630	1 YND1_YEAST	P40009 saccharomyc
22	315.5	13.2	529	1 ENP3_HUMAN	O75355 homo sapien
23	302.5	12.7	616	1 ENP4_HUMAN	O9y227 homo sapien
24	297.5	12.5	613	1 ENP4_MOUSE	O9dbt4 mus musculu
25	162.5	6.8	628	1 NTP2_TOXGO	O27893 toxoplasma
26	160.5	6.7	628	1 NTP2_TOXGO	O27893 toxoplasma
27	143.5	6.0	592	1 NTP4_TOXGO	P52913 toxoplasma
28	124	5.2	524	1 AMPA_AERPE	O9y935 aeropyrum p
29	110.5	4.6	880	1 BGL2_SACRI	P22507 saccharomyc
30	107.5	4.5	891	1 MUTS_RICR	O9zcm9 rickettsia
31	104.5	4.4	349	1 ISPG_CIOAB	O97156 clostridium
32	103	4.3	565	1 SCRI_SCHPO	O14335 schizosacch
33	102	4.3	705	1 PPK_BACHD	O9xd27 bacillus ha

34	101	4.2	531	1	G6P1_SYNT3	P52983 synechocyst
35	100	4.2	546	1	NAOX_ENTRA	P37061 enterococcu
36	99	4.2	483	1	PMEU_LYCES	O43143 lycopersico
37	99	4.2	1092	1	DHE2_YEAST	P33327 saccharomyc
38	98	4.1	2183	1	POLG_CXBAE	O86887 c genome po
39	97	4.1	1050	1	LKTA_ACTAC	P16462 actinobacill
40	96.5	4.1	411	1	YCGP_BACSV	P16462 actinobacill
41	96.5	4.1	1013	1	ALIA3_HUMAN	P13637 homo sapien
42	96	4.0	659	1	ARGA_ECOLI	P37127 escherichia
43	96	4.0	3063	1	CAIC_HUMAN	O99715 homo sapien
44	95.5	4.0	604	1	LEPA_HELPU	O9zcm93 helicobacte
45	94.5	4.0	1010	1	ALIA3_CHICK	P24798 gallus galli

ALIGNMENTS

```

RESULT 1
ID NTPA_PEA
AC P52914:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Nucleoside-triphosphatase (EC 3.6.1.15) (Nucleoside triphosphate
DE phosphohydrolase) (NTPase) (Apyrase).
OS Pisum sativum (Garden pea)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ALASKA; TISSUE=Plumule;
RX MEDLINE=96197404; PubMed=8616230;
RA Hsieh H., Tong C.G., Thomas C., Roux S.J.;
RT "Light-modulated abundance of an mRNA encoding a
RT calmodulin-regulated, chromatin-associated NTPase in pea.";
RL Plant Mol. Biol. 30:135-147(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. Alaska; TISSUE=Stem;
RA Shidpara K., Abe S., Davies E.;
RT "Structure of the coding region and mRNA variants of the apyrase from
RT Pisum sativum.";
RL Acta Physiol. Plant. 20:3-13(2001).
CC -!- FUNCTION: MIGHT BE INVOLVED IN RNA TRANSPORT OUT OF NUCLEI.
CC -!- CATALYTIC ACTIVITY: NTP + H(2)O = NDP + phosphate.
CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEUS.
CC -!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
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CC
CC EMBL: 232743; CAB83655.1; -.
CC EMBL: AB027614; BAB18900.1; -.
CC Interp: IPR000407; GDA1_CD39_NTPase.
CC Pfam: PF01150; GDA1_CD39_1.
CC PROSITE: PS01238; GDA1_CD39_NTPASE; 1.
CC HYDROLASE; Nuclear protein.
CC KW SEQUENCE 455 AA; 50PDP0023ABC4299 CRC64;

```

Query Match 70.3%; Score 1675.5; DB 1; Length 455;
Best Local Similarity 68.7%; Pred. No. 2.2e-117;
Matches 314; Conservative 64; Mismatches 76; Indels 3; Gaps 2;
QY 7 MFLISLMTFVEMLTPAIISSQYLGNNILMNRKILPKNQEPVTSVAVIFDAGSTGSRVH 66

```

Db 1 MELLIKITLITFLFMSPAITSSOYLGNLLTSKRIPL-KQEIISYAVFDGSGTGRH 58
QY 67 YVNFQNDLLVVENLEFYDYKPOLSSYAANPEABSLIPLKEANVVPVSOQPN 126
Db 59 VYFHNMDLHIGKGVENYKNTIPOLSSYANNPEQAKSLIPLLEQADVVDLLOPT 118
QY 127 PVKLGATAGLRLLEGNAANIIOAVDMLSNSALNVSDAIIIDGQEGSYLWVTIN 186
Db 119 PYRLGATAGLRLINDASKIIOAVDMLSNSALNVSDAIIIDGQEGSYLWVTIN 178
QY 187 LGLGKRTKTVGVVDLGGGVSQMTYAVSRNTAKNAPVGEDEPYIKLVLQSKYYL 246
Db 179 ALGNLGGKTKTVGVVDLGGGVSQMAVSKTAKNAKVDGDDPYIKKVLKIPYDL 238
QY 247 YVHSLYRGREAFRAEIRFVAGGSANPCLIGEDGATYYSAGEVYSAPAGSNINOCRK 306
Db 239 YVHSLYHGREASRAEILKLPSPNCLIGFNGIYYSAGEFKAATYTSGANFNCKN 298
QY 307 IALKALKYNAPCPYONCTFGGIMNGGSGOKNLFTSSFYLSBDVG-IFVKNPKAKIR 365
Db 299 TIRKALKINYPCCPYONCTFGGIMNGGSGOKNLFTSSFYLSBDVG-IFVKNPKAKIR 358
QY 366 PYDLTAKTACKTNLEDAKSKYRPLYEKDSVEYVCLDLYVYTLVDGFGLDPEQVTV 425
Db 369 PVDITFAKKEACALNFEDAKSTYPLDKKNVASYCMLDIQYVLLVDGFGLDPEQKITS 418
QY 426 ANEIEYODALVEAAMPGLTGAIEAISLKPFRMLWFEI 462
Db 419 GKEIEYODALVEAAMPGLGNVAEISALPKFERMLWFEV 455

RESULT 2
APY_SOLUTION STANDARD: PRT: 454 AA.
ID APY_SOLUTION STANDARD: PRT: 454 AA.
AC P80595; Q43164;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Aprtase precursor (EC 3.6.1.5) (ATP-diphosphatase) (Adenosine diphosphatase) (ADPase) (ATP-diphosphohydrolyase).
GN ROP1.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 59-160; 236-253 AND 332-345.
RC TISSUE=Tuber;
RX MEDLINE=96158985; PubMed=8579614;
RA Handa M., Guidotti G.;
RT "Purification and cloning of a soluble ATP-diphosphohydrolyase (aprtase) from potato tubers (Solanum tuberosum).";
RL Biochem. Biophys. Res. Commun. 218:916-923(1996).
RN [2]
RP SEQUENCE OF 42-54; 68-95 AND 236-253.
RC STRAIN=CV. DESIREE;
RX MEDLINE=96355615; PubMed=8703025;
RA Vasconcelos E.G., Ferreira S.T., de Carvalho T.M.U., de Souza W., Kettlun A.M., Mancilla M., Valenzuela M.A., Verjovski-Almeida S.;
RT "Partial purification and immunohistochemical localization of ATP diphosphohydrolyase from Schistosoma mansoni. Immunological cross-reactivities with potato aprtase and Toxoplasma gondii nucleoside triphosphate hydrolase.";
RL J. Biol. Chem. 271:22139-22145(1996).
CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF PHOSPHOANHYDRIDE BONDS OF NUCLEOSIDE TRI- AND DI-PHOSPHATES.
CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -1- COFACTOR: CALCIUM.
CC -1- SUBCELLULAR LOCATION: Membrane-associated (Probable).
CC -1- PPM: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.

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CC -----
DR EMBL; U58597; AAB02720.1; -
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39_1.
DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
KW Hydrolase; Transmembrane; Calcium; Signal.
FT SIGNAL 1
FT CHAIN 31
FT TRANSMEM 426
FT CARBOHYD 151
FT CARBOHYD 262
SQ SEQUENCE 454 AA; 50041 MW; 9D9FEFA31DA2F32F CRC64;

Query Match 49.6%; Score 1182.5; DB 1; Length 454;
Best Local Similarity 51.1%; Pred. No. 1,1e-80;
Matches 226; Conservative 85; Mismatches 124; Indels 7; Gaps 4;

QY 11 ISLMTFVFMILPAISSOYLGNILNKRKLLPKNOEPTSYAVIPDAGSTGRVHYNF 70
Db 9 IFILALFVLPPLSLSKNNAQIPLRHLHSESH---YAVIPDAGSTGRVHYNFRF 64
QY 71 DONIDLPLENELEFYDSVPGLSYAAANPEEAESLIPLKRAENVVPSOQPNPVTL 130
Db 65 DEKLGILPIONNIEFYMAHEPGLSTAEDEPKKAANLEPLDGAEGSVQELQSEPLEL 124
QY 131 GATAGLRLEGNAAENILQAVRDMLSNSALNVSDAIIIDGQEGSYLWVTINYLCK 190
Db 125 GATAGLRMLKGDAAEKILQAVRNLVKNOSTFHSKIDQMTILIDGQEGSYMAAINVLGN 184
QY 191 LGRFRTKTVGVVDLGGGVSQMTYAVSRNTAKNAPVGEDEPYIKLVLQSKYYLYHS 250
Db 185 LGRDYSTRTATIDLGGGVSQMAVAISNEOPAKAPQWEDSE-PRVQOKHLMSTDYMLYHS 243
QY 251 YLRGREAFAEIRFVAGGSANPCLIGEDGATYYSAGEYKVSAPAGSNINOCRKALK 310
Db 244 YLWYGLAARAEIFKASRNENPCALGEGDGYYSGVGVYKVKARKKSGSMKRCRLRH 303
QY 311 ALKVNAPCPYONCTFGGIMNGGSGOKNLFTSSFYLSSEVGFVFNK-PAKIRPVDL 369
Db 304 ALKINAKCNIETCTENGWNGGSGDQKNIHASFFFYDGAQVGIYDKRFPALAKPIQY 363
QY 370 KTAAKLACKTNLEDAKSKYRPLYEKDSVEYVCLDLYVYTLVDGFGLDPEQVTVANEI 429
Db 364 LNAKVAQCTNVADIKSIRPKQDR-NIPYLCMDLIYETLLVDGFGINPKHEITIVHDV 422
QY 430 EYODALVEAAMPGLGTAIEAIISS 451
Db 423 QYKNYLVGAAMPGLGCAIDLVSS 444

RESULT 3
ENPS_HUMAN STANDARD: PRT: 428 AA.
ID ENPS_HUMAN STANDARD: PRT: 428 AA.
AC O75356;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Echinucleoside triphosphate diphosphohydrolase 5 precursor
DE (EC 3.6.1.6) (NTPdase5) (Nucleoside diphosphatase) (CD39 antigen-like 4) (ER-UDPase).
GN ENTPD5 OR CD39L4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

```


OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX TISSUE=Leukemia;
 RA MEDLINE=9834119; PubMed=9676430;
 RT Chadwick B.P., Frischaut A.-M.;
 RT "The CD39-like gene family: identification of three new human members
 (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of
 the gene family from *Drosophila melanogaster*.";
 RL Genomics 50:357-367(1998).
 CC -|- FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN
 CC GLYCOPROTEIN FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC
 CC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER
 CC NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE PYROPHOSPHATE
 CC (BY SIMILARITY).
 CC -|- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
 CC nucleotide + phosphate.
 CC -|- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -|- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -|- TISSUE SPECIFICITY: EXPRESSED IN ADULT LIVER, KIDNEY, PROSTATE,
 CC TESTIS AND COLON. MUCH WEAKER EXPRESSION IN OTHER TISSUES.
 CC -|- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
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 CC
 CC -----
 DR EMBL: AF039918; AAC39885.1; -
 DR MIM: 603162; -
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39; 1.
 DR PROSITE: PS01238; GDA1_CD39_NTPASE; FALSE NEG.
 DR HydroLase: Transmembrane; Glycoprotein; Calcium; Magnesium;
 KM Endoplasmic reticulum; Signal.
 FT SIGNAL 1 20
 FT CHAIN 1 428
 FT ECTONUCLEOSIDE TRIPHOSPHATE
 FT DIPHOHODIOLASE 5.
 FT CARBOHYD 42 42
 FT CARBOHYD 232 232
 FT CARBOHYD 368 368
 FT SEQUENCE 428 AA; 47517 MW; 830437A15DE4DD CRC64;
 SQ
 Query Match 20.6%; Score 491.5; DB 1; Length 428;
 Best Local Similarity 31.3%; Pred. No. 3, 1e-29;
 Matches 134; Conservative 71; Mismatches 166; Indels 57; Gaps 14;

DB 321 -----VQSGSFASYYDDRAVDMDIDYEGKILKVEDFERKAREVC-DNLENE 369
 QY 385 KSKYPPDYKDSVEYVCLDYVYTTLLVDFGDPDPEVYVAIEYQALVAPAPLGI 444
 DB 370 TSGSP-----FLCMDLSTYITALLKDGFG--PADSTVL-QLTKVNIETGMALGA 416
 QY 445 AIEAIISSL 452
 DB 417 TFFHLQSL 424
 RESULT 4
 ENPS_MOUSE
 ID ENPS_MOUSE STANDARD; PRT; 427 AA.
 AC 09NUZ9_070214;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor
 DE (EC 3.6.1.6) (NTPases5) (Nucleoside diphosphatase) (CD39 antigen-like
 DE 4) (ER-UDPase).
 GN ENTPD5 OR CD39L4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98119025; PubMed=9457681;
 RA Chadwick B.P., Williamson J., Sheer D., Frischaut A.-M.;
 RT "cDNA cloning and chromosomal mapping of a mouse gene with homology to
 RT NTPases.";
 RL Mamm. Genome 9:162-164(1998).
 RN [2]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION.
 RC TISSUE=Liver;
 RX MEDLINE=99298181; PubMed=10369669;
 RA Trombetta E.S., Melenius A.;
 RT "Glycoprotein reglucosylation and nucleotide sugar utilization in the
 RT secretory pathway: Identification of a nucleoside diphosphatase in the
 RL endoplasmic reticulum.";
 RL EMBO J. 18:3282-3292(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleschmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
 RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carinici P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Morone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyushaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -|- FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN
 CC GLYCOPROTEIN FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC
 CC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER
 CC NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE
 CC PYROPHOSPHATE.
 CC -|- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a

```

CC nucleotide + phosphate.
CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- PM: GLYCOSYLATED WITH HIGH MANNOSE N-LINKED GLYCAN.
CC -1- MISCELLANEOUS: OPTIMAL PH IS NEUTRAL.
CC -1- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
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CC -----
DR EMBL: AF006482; AAC05181.1; -
DR EMBL: AJ238636; CAB45533.1; -
DR EMBL: AK002618; BAB2234.1; -
DR MGI: MGI:1321385; Entpd5.
DR InterPro: IPR000407; GDA1_CD39_NTPase.
DR Pfam: PF01150; GDA1_CD39; 1.
DR PROSITE: PS01238; GDA1_CD39_NTPASE; FALSE_NEG.
KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW Endoplasmic reticulum; Signal.
FT SIGNAL 1 18
FT CHAIN 1 18
FT ECTONUCLEOSIDE TRIPHOSPHATE
FT DIPHOSPHOHYDROLASE 5.
FT CARBOHYD 41 41
FT CARBOHYD 231 231
FT CONFLICT 390 390
FT CONFLICT 394 427
FT FT
FT FT
SQ SEQUENCE 427 AA; 47101 MW; 2F9DA2C342C55577 CRC64;

Query Match 20.1%; Score 479; DB 1; Length 427;
Best Local Similarity 30.0%; Pred. No. 2; 6e-28;
Matches 138; Conservative 74; Mismatches 180; Indels 68; Gaps 16;

QY 17 VEMLPAISSQYLGNNILNMRK-----LILPKNOEPTSYAVIFDAGSTGSRVH 66
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 8 VEMLILAC-----VGVTFYREOQTWEGVFLSMCRPNVSAGTFYIMEDAGSTGTRIH 62
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 67 VYNVDQ-----NLDLPEVNELEFYDSVKGILSYANPEEAESLILPLKEAENVVPSQ 122
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 63 VYTFVQRTAGOLPFL-----EGELFDSVKGILSYANPEEAESLILPLKEAENVVPSQ 118
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 123 QPNTPVKLGATAGRLLEGNAENIILQAVRDMLSNRSALVQSAVSILDTGOGSTLWY 182
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 119 WERTPVYLKATAGRLRPEQAKQMLLEVEITRKN--SPETLVPDGSVIMSGVEGILAWY 177
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 183 TINTLLKIKRFTKTVGVVLDGGSVQMTYAVSRNTAKNAPVSEDEDEYIKKLVLOK 242
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 178 TVNFLTQGLHGRQETVGTDLGASQTITFL--POEKTLEQTPRG---YLISFEHENS 232
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 243 KYDLVYHSYLRKGRFAELFKV--AGGS-----ANPCLLAGDGAITYYSGAEKYSAP 295
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 233 TFKLYTHSYLGFQKARLALTLGLALEAKGDGHTFRSACILPRMLEAWIRGKVGKVGQGN 292
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 296 ASGS--NLNOCRKIALKAL--KVNAPCPYONCTGGIWNNGSGGSKNKLFLTSSFYLSLD 352
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 293 QEGEMGEPEFYAEVLRVQOKLQPEEVKSAF-----YAFSYDYRAAD 337
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 353 VGIFVKNPKAIRPVLDLTAALACKLTNLEDAKSKYPDLEYKDSVEVYCDLVVYVTLVY 412
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 338 THLIDYEKGVLKVEDPERAKREVC--DNLGSFSSGSP-----FLCMDLYITALLK 387
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 413 DGGGLDPQEVYVANELEIYODALVEAAMPGLTAIEAISL 452
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 388 DGGF-----FADGTL--OLTKRVNIIETGMALGATFHLLQSL 423
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

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RESULT 5
ID ENP5_MESAU STANDARD; PRT; 469 AA.
AC 090YCG; 090YCG;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor
DE (RC 3.6.1.6) (NTPDase5) (Nucleoside diphosphatase) (CD39 antigen-like
DE 4) (ER-UDPase) (Proto-oncogene cph).
GN ENTPD5 OR CD39L4 OR CPH.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_Taxid=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99142925; PubMed=9989819;
RA Velasco J.A., Avila M.A., Notario V.;
RT "The product of the cph oncogene is a truncated, nucleotide-binding
RT protein that enhances cellular survival to stress."
RL Oncogene 18:689-701(1999).
CC -1- FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN
CC GLYCOPROTEIN FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC
CC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER
CC NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE PYRIPHOSPHATE
CC (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC nucleotide + phosphate.
CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL CELLS AND MOST ADULT
CC TISSUES.
CC -1- DISEASE: CPH ONCOGENE HAS TRANSFORMING CAPACITY AND TUMORIGENIC
CC POTENTIAL.
CC -1- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF084568; AAF22931.1; ALF_TERM.
DR EMBL: AF084569; AAF22932.1; -.
DR InterPro: IPR000407; GDA1_CD39_NTPase.
DR Pfam: PF01150; GDA1_CD39; 1.
DR PROSITE: PS01238; GDA1_CD39_NTPASE; FALSE_NEG.
KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW Endoplasmic reticulum; Signal; Proto-oncogene.
FT SIGNAL 1 18
FT CHAIN 1 18
FT ECTONUCLEOSIDE TRIPHOSPHATE
FT DIPHOSPHOHYDROLASE 5.
FT CARBOHYD 42 42
FT CARBOHYD 232 232
FT FT
FT FT
SQ SEQUENCE 469 AA; 52125 MW; 03D8A23E0C73474B CRC64;

Query Match 19.6%; Score 468; DB 1; Length 469;
Best Local Similarity 29.5%; Pred. No. 2e-27;
Matches 134; Conservative 76; Mismatches 168; Indels 76; Gaps 16;

QY 18 VEMLPAISSQYLGNNILNMRKILPKNOEPTSYAVIFDAGSTGSRVHYNF 70
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 10 FLIMTACAGSTFYREOQTWEGVFLSS--MCPANVASSTFGIMFDAGSTGTRIHVYTF 67
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 71 DQ-----NLDLPEVNELEFYDSVKGILSYANPEEAESLILPLKEAENVVPSQ 126
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 68 VOKAGQLPFL-----EGELFDSVKGILSYANPEEAESLILPLKEAENVVPSQ 123
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

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OY 127 PVKLGATAGLRLEGNAENIIQAVRDMLSALNVQSDAVSILDGTOEGSYLWITNY 186
RA 124 PVLVATATNRLRLEPKQAQALLLEVEIR-KMSPLVPDSDSINDSGEGLIANTVNF 182
DB 187 LIGKLGKRTKTVGVVDLGGSSVQMTYAVS-RNTAKNAKRVBEGEDPYIKLVLOGKKYD 245
OY 183 LYGOLHGHSEQETMGTDLGASTQITFLPQFSKLEQTRP-----DYLTSEMFNSTPK 236
DB 246 LVHSTLRGRGRFR-----AEIRVAGGSANPCILAGFDATYYSGAEYV 292
OY 237 LKTHSYLGGLKAARLATLGALETCTDCHTRSA-----CLPRWLEAMWIFGKXOY 290
DB 293 SAPASGS-NLNCORKIALKAL--KVNAPCYONCTFGGIMWGGSGQNLFLTSSFYV 349
OY 291 GGNQGEKMEFECYAEVLRVVOGKLLHOPEIRGSSP-----YAFSTYIDR 335
DB 350 SEDVGIFFVNRPAKIRPVDLKTAAKLTNLEDAKSKYPDYEKDSVEYVCLDLYVYT 409
OY 336 AADTHLIDYKGGVLAKEVDFEKAREVC-DNLESFTSGSP-----FLCMDLSYITA 385
DB 410 LLYDGFGLDPFOEVYVANEIEYQDALVEAMPUG 443
OY 386 LKDGSG--FADGTL-QLTKRVNIETGMPDG 415
DB

RESULT 6
ENP6_HUMAN STANDARD: PRT: 484 AA.
ID ENP6_HUMAN
AC 075354; Q9UJD1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 6 (EC 3.6.1.6)
DE (NTPDase6) (CD39 antigen-like 2).
DE ENTPD6 OR CD39L2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RX TISSUE=Keratinocytes;
RC MEDLINE=98341119; PubMed=9676430;
RT "The CD39-like gene family: identification of three new human members
RT (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of
RL Genomics 50:357-367(1998).
RP SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark R.E., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Guillaume R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Lehar E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levasainio M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McComachie L.J., McIay K., McMurtry A.A.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.E.,
RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,

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RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.:
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -I- FUNCTION: MIGHT SUPPORT GLYCOSYLATION REACTIONS IN THE GOLGI
CC APPARATUS AND, WHEN RELEASED FROM CELLS, MIGHT CATALYZE THE
CC HYDROLYSIS OF EXTRACELLULAR NUCLEOTIDES. HYDROLYZES PREFERENTIALLY
CC NUCLEOSIDE 5'-DIPHOSPHATES. NUCLEOSIDE 5'-TRIPHOSPHATES ARE
CC HYDROLYZED ONLY TO A MINOR EXTENT. THERE IS NO HYDROLYSIS OF
CC NUCLEOSIDE 5'-MONOPHOSPHATES. THE ORDER OF ACTIVITY WITH DIFFERENT
CC SUBSTRATES IS GDP > UDP > CDP > ADP (BY SIMILARITY).
CC -I- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC nucleotide + phosphate.
CC -I- CORRECTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI. BUT ALSO
CC OCCURS IN A SOLUBLE EXTRACELLULAR FORM (BY SIMILARITY).
CC -I- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES.
CC -I- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
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CC -----
CC EMBL; AF039916; AAC39883.1; -.
CC EMBL; AL035252; CAB41571.1; -.
CC MIM: 603160; -.
CC DR InterPro: IPR000407; GDAL_CD39_NTPase.
CC DR Pfam: PF01150; GDAL_CD39_1.
CC DR PROSITE: PS01238; GDAL_CD39_NTPASE; FALSE_NEG.
CC KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium;
CC Signal-anchor; Golgi stack.
CC FT DOMAIN 1 39 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 40 60 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT LUMENAL (POTENTIAL).
CC FT CARBOHYD 220 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 138 138 V -> L (IN REF. 2).
CC FT CONFLICT 202 202 E -> K (IN REF. 2).
CC FT SEQUENCE 484 AA; 53233 MW; 27334B290DB064C CRC64;
CC

Query Match 19.4%; Score 463; DB 1; Length 484;
Best Local Similarity 31.3%; Pred. No. 4, 9e-27;
Matches 131; Conservative 70; Mismatches 156; Indels 62; Gaps 13;
OY 52 YAVIPAGSTGSRVHYNYNDONIDLLPENELEFYTSVYRPGSSYANPEEAESILPLL 111
RA 102 YGIMFAGSTGVRHFEQTRPREPTPLTH-ETFAVAVRGLSAYADVDSKQAGIRELL 160
DB 112 KEAEENVVPVSOQNTFPVKIGATAGLRLEGNAENIIQAVRDMLSALNVQSDAVSIL 171
OY 161 DVAKQDIPDPDKATPLVLKATAGLRLLPEKRAQKLLQKVEVF-KASPLVQDDCVSLM 219
DB 172 DGTQEGSYLWITNYLLGKLGKRTKTVGVVDLGGSSVQMTYAVSRNTAKNAKRV----- 226
OY 220 NGTDEGVSAWITINFLTGLSKTPGSSVGMLDLGGSGSTQIAF-----LPRVGTQL 270
DB 227 --PEGDPIYIKLVLOGKKYDLYVHSYLYKGRAPFAELFKVAGGS-----ANPCIL 276
OY 271 ASPPG---LTLRLMRNRYKLYSYSLDGLMSALATLGGVEGPPARDGKELVSPCL 327
DB 277 AGPDGAVTYSAGAEYKYSAPASGSNLNO-CRKIALKAL--KVNAPCYONCTFGGIMWGG 333
OY 328 PSKGSWEIAEYTYRYSQKAASLHELCAARSEVLQKRVHRTTEVKYHDF----- 379
DB 334 GSGQKNLFTLTSFYVLSDEVGIFVNRPAKIRPVDLKTAAKLTNLEDAKSKYPDLYE 393

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CC -1- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
CC -----
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CC -----
DR EMBL; L19560; AAA34656.1; -
DR EMBL; U18779; AAB65000.1; -
DR PIR; S30837; S30837.
DR PIR; A40732; A40732.
DR SGD; S0000768; GDAL1.
DR InterPro; IPR000407; GDAL1_CD39_NTPase.
DR Pfam; PF01150; GDAL1_CD39; 1.
DR PROSITE; PS01238; GDAL1_CD39_NTPASE; 1.
KW Hydrolase; Golgi stack; Glycoprotein; Transmembrane; Signal-anchor.
FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 10 24 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT LUMENAL (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 518 AA; 56821 MW; 9A61182D5ED22ADF CXC64;

Query Match 18.68; Score 442.5; DB 1; Length 518;
Best Local Similarity 29.18; Pred. No. 1.8e-25;
Matches 153; Conservative 70; Mismatches 178; Indels 125; Gaps 20;

QY 17 VPMMLPAISSQY-----LGNNTIMRKLT-----LLPKNDP----- 48
DB 17 VIMLILKTSIGPPSARTVTPNASIPKTPEDISILPVNDEPYLDQSKTEQYPELA 76
QY 49 -----VTVFADAGSGSRVHYNFD-----QNDLDPVENELFFYDSV 89
DB 77 DAVKQTSQTSSEHKYIYIMDAGSGSRVHYNFDVCTSPPTLD-----EKFDWL 128
QY 90 KPGLSYVAMPDEEAESLIPLKEANVYVSOQPTPVKLGATAGLRLEGNAENITIQ 149
DB 129 EPGLSFPTDSVGANSIDPLTKVAMNYVPIKARCTPVAVAKATAGRLGLGAKSKILS 188
QY 150 AVRODLNRSALN-VQSNVSTLOTOGSGYMTINILGLKGRPRK--TVGVVDLGG 206
DB 189 AVRODLERDYPPEVVEGGVSGVSMGDEGVFAMITNTNLLGNIGANGRLPTAAVFDLGG 248
QY 207 GSVQNTYAVSRNTAKNAKPEDEDPYIKKLVLOGKKYDLVHSYLRYGREAFAEIRKY 266
DB 249 GSTQIVF---EFTFPINERKMDGEHKF--DLKFGDENTLVQSHLGGKGRKRVKSV 303
QY 267 AGGSA--NPCILAGFDGYATYSGAERYKVASAPASGSLN----- 302
DB 304 LVENALKDKGKILKG-DNMTKT-----HQLSSPCLPKPVNATNEKYTVLESKEFYTIDFIPGD 357
QY 303 -----QCRKIALKALKVNAPCYONCTFGITWNG-----GGSQKMLFLTSSYYIASEDVG 354
DB 358 EPGSAQCRFLDELILNKDAQCPSCSFNGVQPSLVFTKESNDIYIFSYFYDTRPLG 417
QY 355 IFVNKNPKAKIRPV-----DLTKAALACKTNLEDAKSKYP-----DLYEKDSVEYVCLDIY 405
DB 418 M-----PLSFTLMEINDLARIYCKGE-ETWNSVFSGAGSLDELIESHSRHCLOLS 466
QY 406 VYTTLLVDGFGIDPFQEVTVANEIEYODALVEAMPICGTAIEAISS 451
DB 467 EQVSLHTGVDIPIDQRELRTGKRI-----ANKETGICGLASISPLLKA 508

RESULT 9
ENPL_RAT STANDARD; PRT; 511 AA.
ID ENPL_RAT

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AC P97687;
DR 16-OCT-2001 (Rel. 40, Last sequence update)
DR 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NMPDase) (ecto-ATP diphosphohydrolase) (ATPDase) (lymphoid cell
DE activation antigen) (CD39 antigen) (Ecto-apyrase).
GN ENTPD1 OR CD39.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain, and Hippocampus;
RX MEDLINE=96215267; Pubmed=8626624;
RA Wang T.-F., Rosenberg P.A., Guidotti G.;
RT "Characterization of brain ecto-apyrase: evidence for only one ecto-
RT apyrase (CD39) gene.";
RL Brain Res. Mol. Brain Res. 47:295-302(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Mistar; TISSUE=Cochlea;
RX MEDLINE=20050856; Pubmed=10581401;
RA Vlakovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
RT "Evidence for alternative splicing of ecto-ATPase associated with
RT termination of putinergic transmission.";
RL Brain Res. Mol. Brain Res. 73:85-92(1999).
RN [3]
RP SEQUENCE OF 432-511 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=98031057; Pubmed=9364474;
RA Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
RT "An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
RT rat brain.";
RL Neuroparmacology 36:1189-1200(1997).
CC -1- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
CC NUCLEOTIDES TO REGULATE PURINERGIC NEUOTRANSMISSION. COULD ALSO
CC BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
CC HYDROLYZES ATP AND ADP EQUALLY WELL.
CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O -> AMP + 2 phosphate.
CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN PRIMARY NEURONS AND ASTROCYTES,
CC KIDNEY, LIVER, MUSCLE, THYMUS, LUNG AND SPLEEN.
CC -1- PTM: N-GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U81295; AAC53195.1; -
DR EMBL; Y15685; CA475730.1; -
DR InterPro; IPR000407; GDAL1_CD39_NTPase.
DR Pfam; PF01150; GDAL1_CD39; 1.
KW PROSITE; PS01238; GDAL1_CD39_NTPASE; 1.
KW Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 17 37 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 38 478 POTENTIAL.
FT TRANSMEM 479 499 POTENTIAL.
FT DOMAIN 500 511 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL)
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
 FT CONFLICT 332 332 F -> L (IN REF. 2)
 SQ SEQUENCE 511 AA; 57408 MW; 4CC123D3E644C193 CMC64;

Query Match 17.8%; Score 424; DB 1; Length 511;
 Best Local Similarity 28.1%; Pred. No. 4.2e-24;
 Matches 132; Conservative 70; Mismatches 163; Indels 104; Gaps 22;

OY 42 LPKNGEPTVSIVIPDASTGSRHVAVYFNDQMLLPVENE-----LEFYSVKPGI 93
 DB 43 LPEN-----VKIGIVLDAGSSHTNLYIKW-----PAKENDGTGYVQLLECCVKGPGI 91
 OY 94 SSYAANPEAEASLILPLKEAENVVPSQDNTPYKIGATAGLRLL-----EGNAENITQA 150
 DB 92 SKYAAKTDEIAVYLAECCKMSTERIPASKQOTYVYICATIGMRLRRESKOSADAVYAA 151
 OY 151 VRDMISNSALNVOSD-AVSILDGTGSGYLWYINYLGLKGRFRK----- 197
 DB 152 V-----SRSLKSPFDEFGAKITGQEGAGYGMITINLLG-----RFTQEGSWINFI SDS 202
 OY 198 -----TVGVVDGGGSGVOMTVAVSNRTAKNAKVPEDGPYIKLVLOGKTYLVHSYLR 253
 DB 203 OKQATFGALDGGSSSTOYTF-VPLNQGLEAPETS-----LQRLYGTDTYVYTHSFLC 254
 OY 254 YGREAF-----RAEIKVYAGGS--ANPCILAGFDGATYTSGA-----EYK 291
 DB 255 YGKDQALMOKLAODIQYSSGGLMDPCFYPKYKVVAVSELYGPGCKRREKILPEWFOQ 314
 OY 292 VSAASGSNLNOCCKIKALKVNAPCPYONCTFFGIGW-----NGGGSGGKNLELTSSPY 347
 DB 315 VQGT-----GDVEQCHQSILKFEFN-NSHCPYSQCAFNGVFLPLDQSGFSA-----FSAFY 363
 OY 348 YLSEDVGIFVKKPAKIRPYDLKT-AAKLCKTNLEDAKSKYPRLYDSVEVYCLDLYV 406
 DB 364 FVMD-----FFKKMANDSVSDEKTEIRKNCSEKRWEEVKAStPYKVKYLSER-CESGTY 419
 OY 407 VYTLVVGFGIDPEQEVYVANEIEYODALVE--AAMPDGAIPAISLSP 453
 DB 420 ILTLLDGGYNETG-----TSMQIHFMGKIKDINSAGWTLGYMLNLJTMIP 464

RESULT 10
 ENPL_HUMAN STANDARD; PRT; 510 AA.
 AC P49661; Q9U0Q9; Q9Y3Q9;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 DE (NTPase) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
 DE activation antigen) (CD39 antigen) (Ecto-apyrase).
 GN ECTP1 OR CD39.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RX SEQUENCE FROM N.A. (ISOFORM VASCULAR).
 RX MEDLINE=95015846; PubMed=7930580;
 RA Maliszewski C.R., Dellespesse G.J.T., Schoenborn M.A., Amftige R.J.,
 RA Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,
 RA Birks C., Albert A., Friend D., Gimpel S.D., Gayle R.B. III;
 RT "The CD39 lymphoid cell activation antigen. Molecular cloning and
 RT structural characterization."
 RL J. Immunol. 153:3574-3583(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM VASCULAR).
 RC TISSUE=umbilical vein;
 RX MEDLINE=97149443; PubMed=8996251;
 RA Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Kozlak K.,
 RA Millan M., Hancock W.W., Bach F.H.;

RT "Loss of ATP diphosphohydrolase activity with endothelial cell
 RT activation.";
 RT J. Exp. Med. 185:153-163(1997).
 RL [3]
 RP SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND II).
 RC TISSUE=Placenta;
 RX MEDLINE=99332082; PubMed=10405171;
 RA Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,
 RA Titani K., Fujimura Y., Narita N.;
 RT "The CDNA cloning of human placental ecto-ATP diphosphohydrolases I
 RT and II.";
 RL FEBS Lett. 453:335-340(1999).
 RN [4]
 RP SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.
 RC TISSUE=Placenta;
 RX MEDLINE=96096723; PubMed=8529670;
 RA Christoforidis S., Pamaracki T., Galaris D., Kellner R., Tsolas O.;
 RT "Purification and properties of human placental ATP
 RT diphosphohydrolase.";
 RL Eur. J. Biochem. 234:66-74(1995).
 RN [5]
 RP SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND
 RP 399-405 (ISOFORM PLACENTAL I).
 RC TISSUE=Placenta;
 RX MEDLINE=99062444; PubMed=9846014;
 RA Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N.,
 RA Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.;
 RT Placental ecto-ATP diphosphohydrolase: its structural feature
 RT distinct from CD39, localization and inhibition on shear-induced
 RT platelet aggregation.";
 RL Int. J. Hematol. 68:297-310(1998).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=97115858; PubMed=8955160;
 RA Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
 RA Beaudoin A.R., Bach F.H., Robson S.C.;
 RT "Identification and characterization of CD39/vascular ATP
 RT diphosphohydrolase.";
 RL J. Biol. Chem. 271:33116-33122(1996).
 CC -1- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
 CC NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO
 CC BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
 CC HYDROLYSES ATP AND ADP EQUALLY WELL.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED (BY SIMILARTY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC I AND PLACENTAL II; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY ON ACTIVATED LYMPHOID
 CC CELLS. ALSO EXPRESSED IN ENDOTHELIAL TISSUES. THE VASCULAR ISOFORM
 CC AND THE PLACENTAL ISOFORM II ARE PRESENT IN BOTH PLACENTA AND
 CC UMBILICAL VEIN, WHEREAS PLACENTAL ISOFORM I IS PRESENT IN PLACENTA
 CC ONLY.
 CC -1- PTR: THE N-TERMINUS IS BLOCKED.
 CC -1- MISCELLANEOUS: OPTIMAL PH IS 7.0-7.5 WITH ATP AS SUBSTRATE AND
 CC 7.5-8.0 WITH ADP.
 CC -1- SIMILARITY: BELONGS TO THE GDP / CD39 NTPASE FAMILY.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD39 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd39.htm".
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 CC EMBL: S73813; AAB32152.1; -
 CC EMBL: U87967; AAB47572.1; -
 CC EMBL: AJ133133; CAB41886.1; -
 CC EMBL: AJ133134; CAB41887.1; -

DR MIM: 601752; -
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39: 1.
 DR PROSITE: PS01238; GDA1_CD39_NTPase: 1.
 KW Hydrolyase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium;
 KM Alternative splicing.
 FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 38 478 POTENTIAL.
 FT TRANSMEM 479 499 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 500 510 POTENTIAL.
 FT CARBOHYD 73 73 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT VARSPLIC 272 299 I AND ISOFORM PLACENTAL II).
 FT VARSPLIC 272 299 VASNEILRDPCHPGYKRVVNSDYKT -> ASITGSRPA
 PETSAPAPTSCELFQIQ (IN ISOFORM PLACENTAL II).
 FT VARSPLIC 300 510 MISSING (IN ISOFORM PLACENTAL II).
 FT CONFLICT 57 58 SS -> G (IN REF. 5).
 FT CONFLICT 162 162 D -> K (IN REF. 4).
 FT CONFLICT 208 208 T -> TGET (IN REF. 5).
 FT CONFLICT 248 248 V -> Y (IN REF. 5).
 FT SEQUENCE 510 AA: 57964 MW: BAD87D2493649159 CRC64;

Query Match 17.7%; Score 421.5; DB 1; Length 510;
 Best Local Similarity 27.4%; Pred. No. 6.5e-24;
 Matches 126; Conservative 73; Mismatches 174; Indels 87; Gaps 19;

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 DB 43 LLEN-----VKYGIIVDAGSHSLYIKV-----PAKENDTGAVHVEGRVKGPGI 91
 QY 94 SSYANPEEASLSPLPLKEAVNVVVSQPMTPYKLGATAGLRLEGNA---AENILQA 150
 DB 92 SFYQKVNIEIGIYLDCHMERAREVPRSOHETPYLGTAGKRLRMESEELADRVLY 151
 QY 151 VEDMLSNRSALNVQSDAVIDLGTQGSYLWYINLYLGLKLRFE-----TKT 198
 DB 152 VERSLSN---YPEFGGARITIGGEGAGVMTITVLLKFSQGTWESIVPETNNGT 208
 QY 199 VGVVDLGGSVQMTAVSNNTAKNAKVPGEDEPYTKKLVLDGKKDYLVHSLKRGRA 258
 DB 209 FGALDLGGASTQVTPVPOQTIES-----PDN---ALQRLYKQDVNVYTHSLCYGKDO 260
 QY 259 F-----RAEIFKVAAGS--ANPCILAGFDGAVYISG-----AEYVSA PASG-----S 299
 DB 261 AIMOKLAKIOYASNEILDPCHFGYKRVVNSDYLYKTPCKRKRFMTLPFOQFETIGIG 320
 QY 300 NLNOCRKILKALKVNAFCPYONCTFGGIM---NGGGSGGKNLFLTSSFYILSDVGI 355
 DB 321 NVOQCHQSITLLEFNYSY-CFYSQCAFNGFLPPLGGDRFA-----FAFTFVAK----- 368
 QY 356 FVNKNPAKIRPVDLTAARLACKTNLEDAKSKYPDLVERDSEYVCLDLYVYVYTLAVDG- 414
 DB 369 FLNLTSEKVSQEKVEMMKFCAQPMEEIKTSYAGVKEKYLEY-CFSGTYILSLLDGY 427
 QY 415 -FGDLPQEVYVANEIEYODALVEAAMPGLTAIEAIISSLP 453
 DB 428 HFTADSWEHIHFTIGKIGSD---AGWTLGMYLMTLNTMIP 463

RESULT 11
 ENPI_MOUSE STANDARD; PRT; 510 AA.
 AC P55772;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 DE (NTPdase1) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
 DE activation antigen) (CD39 antigen) (Ecto-apyrase).
 GN ENTPD1 OR CD39.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95015846; PubMed=7930580;
 RA Maliszewski C.R., Delaespense G.J.T., Schoenborn M.A., Arnltage R.J.,
 RA Fawlow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,
 RA Barks C., Albert A., Friend D., Gimpel S.D., Gayle R.B. III:
 RT "The CD39 lymphoid cell activation antigen. Molecular cloning and
 RT structural characterization."
 RT J. Immunol. 153:3574-3583(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=98399871; PubMed=9730622;
 RA Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J.,
 RA Gayle R.B. III, Maliszewski C.R.;
 RT "Gene structure and chromosome location of mouse Cd39 coding for an
 RT ecto-apyrase."
 RL Cytogenet. Cell Genet. 81:287-289(1998).
 CC -I- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
 CC NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO
 CC BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
 CC HYDROLYSES ATP AND AD EQUALLY WELL.
 CC -I- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
 CC -I- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).
 CC -I- SUBUNIT: HOMODIMER. DISULFIDE-LINKED (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -I- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF037366; AAB92259.1; -
 CC EMBL: AF041818; AAC83203.1; -
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 CC EMBL: MGI:102805; Entpd1.
 DR MGD: MGI:102805; Entpd1.
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39: 1.
 DR PROSITE: PS01238; GDA1_CD39_NTPase: 1.
 KW Hydrolyase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium;
 KM Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 38 478 POTENTIAL.
 FT TRANSMEM 479 499 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 500 510 POTENTIAL.
 FT CARBOHYD 73 73 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 428 428 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
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Query Match 17.2%; Score 410.5; DB 1; Length 510;

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 00:42:50 ; Search time 254.74 Seconds
(without alignments)
10035.666 Million cell updates/sec

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Perfect score: 1489
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched:      1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 34728722
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1479.6	99.4	1489	20	AAK08529	NBP46 (root lectin
2	869.2	58.4	1458	20	AAK08528	NBP46 (root lectin
3	839.8	56.4	1661	21	AAA96064	Ecto-phosphatase c
4	835	56.1	1667	22	AAF85681	Pea blight resistar
5	833.4	56.0	1697	22	AAF85680	Pea blight resistar
6	830.4	55.8	1368	22	AAF85679	Pea blight resistar
7	824.6	55.4	1643	20	AAK08522	NBP46 (root lectin
8	646	43.4	1434	20	AAK08530	DBX oligosaccharid
9	451.6	30.3	1981	21	AAK39492	Arabidopsis thaliaa

10	441.4	29.6	1530	21	AAA66075	Potato lectin
11	164	11.0	6265	20	AAH08451	NBP6 (root lectin)
12	91.2	6.1	1287	22	AAE63402	Human CD39 like pr
13	91.2	6.1	1601	21	AAE50358	Human CD39-L66 pro
14	91.2	6.1	1601	21	AAE63384	Human CDNA encodin
15	91.2	6.1	1799	21	AAE250356	Human CD39-L4 prot
16	91.2	6.1	1799	22	AAE63383	Human CDNA encodin
17	91.2	6.1	1998	21	AAE60658	Human ecto-phosphat
18	84.8	5.7	1287	21	AAE50357	Human CD39-L4 vari
19	84.8	5.7	1287	22	AAE63385	DNA encoding human
20	70.6	4.7	1574	23	ABL18793	Drosophila melanog
21	70.6	4.7	1587	23	ABL05589	Drosophila melanog
22	70.6	4.7	3901	23	ABL18792	Drosophila melanog
23	70.6	4.7	5987	23	ABL05588	Drosophila melanog
24	60	4.0	1498	22	AAE63387	cDNA encoding matu
25	60	4.0	1588	22	AAE63433	Human CD39-L2 spli
26	60	4.0	2693	22	AAE63418	Human CD39-L2 spli
27	60	4.0	2762	21	AAE60656	Human ecto-phosphat
28	60	4.0	2762	21	AAE63386	Human CD39-L2 codi
29	60	4.0	2762	22	AAE63422	Human CD39-L2 spli
30	60	4.0	2805	22	AAE63430	Human CD39-L2 spli
31	60	4.0	2882	22	AAE63424	Human CD39-L2 spli
32	56.8	3.8	2564	22	AAK54892	Human full-length
33	51.8	3.5	743	22	AAK91746	Human CDNA 5'-end
34	51.8	3.5	743	22	AAK93764	Human cDNA clone r
35	50	3.4	799	22	AAI22957	Human breast cancer
36	48	3.2	1365	21	AAAD00201	Fusion construct o
37	48	3.2	1365	21	AAAD00206	Human soluble CD39
38	48	3.2	1437	21	AAAD00202	Coding region of p
39	48	3.2	1437	21	AAAD00207	Human soluble CD39
40	48	3.2	1464	21	AAAD00204	Coding region of s
41	48	3.2	1464	21	AAAD00209	Human soluble CD39
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43	48	3.2	1599	21	AAAD00205	Human soluble CD39
44	48	3.2	1704	21	AAE60659	Human ATP diphosph
45	48	3.2	1818	17	AAE63966	DNA coding for hum

ALIGNMENTS

AAx08529
ID AAx08529 standard; cDNA; 1489 BP

AC AAX08529;

XX NBP46 (root lectin) cDNA.
DE

KW NBP46, lectin; rhizobium; leguminous plant; transgenic plant;
KW nitrogen; nitrogen fixation; fertilizer; ss.

Lotus japonica

FH	Key	Location/Qualifiers
25	25	25

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FT      /product="NBP46 root lectin"
FT      misc_feature 700..702
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FT	"/note="	"These bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering given in the specification for this sequence"
FT		
FT		
FT		
FT		

FT/note- "These bases represent nucleotides missing
FT from the sequence given in the specification
FT They are included to maintain the nucleotide
FT numbering given in the specification for this

[illegible]

Query Match	99.48;	Score 1479.6;	DB 20;	Length 1489;
Best Local Similarity	99.3%;	Pred. No. 0;		
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Db	1 aagtcctctctcctcctgagtgatgaattgacttggactaaagcagatgacttcttaattagt	60		
QY	61 ctcatgacotttgytgltcaatgyltaatgctgcgtatctctctccccaatatctcggaac	120		
Db	61 ctcatgacotttgytgltcaatgyltaatgctgcgtatctctctccccaatatctcggaac	120		
QY	121 aacattccatcgaatcgtgaagatattactcccccaaaaatcagaacacgtttacatcatac	180		
Db	121 aacattccatcgaatcgtgaagatattactcccccaaaaatcagaacacgtttacatcatac	180		
QY	181 gctgtatatttgatgcgcgtgtagcacttggaaacgaagccatgcttaaatttttag	240		
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QY	1021	ggtggaagtgtgtccaataaaatcttttccttactcaatcttctatcactctctgaagat	1080
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Db	1141	gctaaactagctctgttaaaaacaaactcttgggaatgcaaaaatcccaataccaagatctt	1200
QY	1201	gggaagaagaagtggtgaatatgtgtgtgtgacattctgttctaagvtgacaacattgctgt	1260
Db	1201	gggaagaagaagtggtgaatatgtgtgtgtgacattctgttctaagvtgacaacattgctgt	1260
QY	1261	gatggaattgtgcttgatccaattccaagaagttacagttggcgaaatgaaatgaaatcaag	1320
Db	1261	gatggaattgtgcttgatccaattccaagaagttacagttggcgaaatgaaatgaaatcaag	1320
QY	1321	gatgtctctgtvgaaagccgcatggtgcctabgagcactgcacatagaagaacatcatcat	1380
Db	1321	gatgtctctgtvgaaagccgcatggtgcctabgagcactgcacatagaagaacatcatcat	1380
QY	1381	cctaatttgaagaatgaatgaatttttaataacttaatactagtactgtttaagctgta	1440
Db	1381	cctaatttgaagaatgaatgaatttttaataacttaatactagtactgtttaagctgta	1440
QY	1441	tactcgaagaataataatgaaataaaagccgcatctttcttccttgctt 1489	

```

Db      1441 taccctgaagaataaatgaaataaagcgcacattcttccttgcctt 1489
|||||
RESULT 2
ID      AAX08528
XX      AAX08528 standard; cDNA: 1458 BP.
XX
XX      AAX08528;
XX
DT      19-JUL-1999 (first entry)
XX
DE      NBP46 (root lectin) cDNA.
XX
XX      NBP46; lectin; Rhizobium; leguminous plant; transgenic plant;
KW      nitrogen; nitrogen fixation; fertilizer; ss.
XX
OS      Medicago sativa.
XX
Key     Location/Qualifiers
FT CDS           complement(1..1380)
FT FT            /tag= a
FT FT            /product= "NBP46 root lectin"
XX
PN      WO9907223-A1.
XX
PD      18-FEB-1999.
XX
PE      05-AUG-1998; 98WO-US16261.
PR      06-AUG-1997; 97US-0907226.
PA      (RBCG ) UNIV CALIFORNIA.
PI      Etzler ME, Murphy JB;
DR      WPI; 1999-167136/14.
DR      P-PSDB; AAW85685.
XX
PT      New polynucleotides encoding Nod factor binding lectins - useful
PR      for production of transgenic plants which are able to fix nitrogen
PS      Example 2; Pages 49-51; 57pp; English.
CC
CC      The NBP46 root lectin is instrumental in recognising and binding
CC      to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate
CC      interaction. The production of transgenic plants comprising an
CC      expression cassette expressing the NBP46 root lectin is advantageous
CC      since it would mean that non-leguminous plants could fix nitrogen
CC      from the atmosphere, lessening the need for the addition of nitrogen
CC      containing fertilizer to soil. This would lead to higher crop yields
CC      where soil has been overplanted and replenishment of the depleted
CC      soil with usable nitrogen. Alternatively, expression of NBP46 can be
CC      used to modulate oligosaccharide signalling in the plant. The nucleic
CC      acid sequences can be used to inhibit expression of an endogenous
CC      gene and also to suppress endogenous NBP46 gene expression.
SQ
Sequence 1458 BP; 438 A; 268 C; 308 G; 444 T; 0 other:

Query Match          58.4%; Score 869.2; DB 20; Length 1458;
Best Local Similarity 77.2%; Pred. No. 1.7e-237;
Matches 1112; Conservative 0; Mismatches 313; Indels 15; Gaps
4;

QY      34 actaagcacatgactttcttaattgtctcat---gaccttggttcatgttaagtcc 90
    ||||| ||||| ||| ||||| |||||   || ||| | || ||||| |||||
DB      4 actaagaacatggagtlcctaattacacatcgcaacttttactctgttaagtcc 63
QY      gttactctctccccaataatcggaaaacaacatctcataacgtaagaattactac 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB      64 gaatcacctctctcccaaratattaggaaaacaacctactaccatcgaagaagttt---- 119
QY      151 cccaanaatcaggaaacagttatcatcataagctgttatatttgatgctgtgatcactgga 210

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Dd	120	--ccaaaacagaacacttaaccttaagcgtgtaacatttgacgctgtagaacgct	177
Qy	211	agcagagatcccatgctctcaaaatttltgatacgaacttgaatctctccgttggaaaacgaa	270
Dd	178	actcgtgtccatgtttacccaatttggatacgaacttaacttaacttcaacttggcaatgat	237
Qy	271	cttgagtttatgtatcgcgtttaaaccggttttgagttcaacgctgtatacctctgaagaa	330
Dd	238	attgagtttgttgacaagatccaacacggttttgagctatggtggatatacttcaacaa	297
Qy	331	gctgcagaatctctgatatccacttctaaaaagacgaagaatgtgttccctgtgacgag	390
Dd	298	gcaacgaaatctctcatctccactcttggaggaagcagaagatgtgtcttcctgaagatctg	357
Qy	391	caaccccaacacacccgtttaaagcttgggacacgtgcaggttttaagctttingaaggat	450
Dd	358	caccccaaaaaaaccccttaagcttggggacacccgcaggttttgaggtcttggatgggagt	417
Qy	451	gctgctgaaaaatatatgtcaacgctgtcaagcgtgtcaggtatgctacgaacagaagtcccttaat	510
Dd	418	gctgctgaaaaagatatgtgcaacgacaggaatattgtcagacaagaagttaacctcaac	477
Qy	511	gttcaatcagatgtagatattatcttgatgtgaacccaagaagttctatccttggtg	570
Dd	478	gttcaacgtgtatgcaagttctatattatgtatgtgaacccaagaagttctatatagtgtg	537
Qy	571	acaattactctctctcgtggggaagttgggaaaaagtttaacagaacggtggagtagt	630
Dd	538	acagttactctatgtatctggggaatcttgggaaaaagcttccacaacaaacagttggagtaact	597
Qy	631	gactgaagaggttggltcagtcagcacaatagacatagccttccaaagaaacacagctctaaat	690
Dd	598	gaccttgaggttggltcagttcaatagacatgtcagctgtcaagaagaacagcaaaaat	657
Qy	691	gtctcaaaagtactgtgaaggaagagatccaataaagaagctgttactccaagggaaag	750
Dd	658	gtctccaaagttgtctgtatgagagagatcccatatataaagaacgtgtgtctcaagggaaag	717
Qy	751	aaatgtgaccttttgttccacagtttacttgcgtatgtgaaggaagacatttgcgtcaag	810
Dd	718	caatatgtctctatglttccaaatctcctgtgcgttlttggacaagaagcaacttgcgaacag	777
Qy	811	atttcaaggtcgcgttgggttgcctgtcaatcccttgcatttttagcgcgtctttagatgggca	870
Dd	778	gttttgaaatgaactaatgtatgtatcgtcaaccttgcattttacccggtattaatgggacc	837
Qy	871	tatacatattccggagcagagatbaaggtctcgcccaagcttccagatctaactgaat	930
Dd	838	tttcaatatccaagagtgaggtataaagcttlttccctcttcttgcgtcccaactttgat	897
Qy	931	caatgtcgaagaagatagctctttaaagcgtcctttaaagtgtagacacgttgcacctatcagat	990
Dd	898	gattgtcaagaagaataattctttaaaggttctttaaagtaaatagatccatgttcccatccggt	957
Qy	991	tgcaactttgtatggagatagtgaaatgtgtgaaggtgtgaagtggtgtccaanaaaatcttccct	1050
Dd	958	tgcaactttgttggataatgagatgtgtgggggggaggtgggcaaaaaaacttttgt	1017
Qy	1051	acttcaatcttctatattacctctctctgaagaatgttggagcttctgtc---aataaaccaat	1107
Dd	1018	acttcaagttctgccttaccctgcgtcgtgaagatgtgtgtatgttggaccaataaactaat	1077
Qy	1108	ggcaaaattgttccagtttgatttgaagacgtgcgcgtcaaaactgtgttgaanaaaactt	1167
Dd	1078	tccaaatacttcatccagtagatttccgaatttgaagacgtcaaaagcgtcttggatcaataactt	1137
Qy	1168	gagagatgcaaaatccaaatacccaagatctttaaagaaagacaggtttgaatatgtgtc	1227
Dd	1138	gagagtgcaaatccactactctccgtcagacttaagtgatgcaaaaag---tccatatgtatgc	1194
Qy	1228	ttgagacttgtctacgctgtacacatgtgctgttgaatgtatgtgtcgttgaatcttcaa	1287

Db 1195 atgatactctatcccaacatgctgtctgttcaatgtgattggcttagtcccgaaaa 1254
Qy 1288 gagttacagtgycgaatgaattgaatcatcagatgctctgttggagccgacgtgctt 1347
Db 1255 gagttacagtgagtgagtggaattcattcatcagatctgttggagctgacgtgctt 1314
Qy 1348 ctgagcactgcacatagaagaatcatcattgcttaattggagattatgtattt 1407
Db 1315 ctgagtgactgcgcgtgagacatcagcgttaccttaagttaagtgattatgtattt 1374
Qy 1408 atttaactactagtgactgttcaagctgattactctgagaataataatgaataaa 1467
Db 1375 atttaagcttttagatagatcgaagataatttcagtaacagcttaacttacaataaa 1434

RESULT 3

AAA96064
ID AAA96064 standard; DNA; 1661 BP.

AC AAA96064;

XX 29-JAN-2001 (first entry)

DE Ecto-phosphatase coding sequence.

XX Ecto-phosphatase; drug resistance; ATP gradient; chemotherapeutic;
KW antibiotic; herbicide; extra-cellular phosphatase; ds.

OS Pisum sativum.

PN WO200052144-A1.

PD 08-SEP-2000.

PF 28-FEB-2000; 2000MO-US05315.

PR 03-MAR-1999; 99US-0261825.

PA (TEXA) UNTV TEXAS.

PI Thomas CE, Wlndor JB, Roux SJ, Lloyd AM, Hurley L;

DR WPI; 2000-587306/55.

XX Increasing or decreasing drug resistance in target bacteria, yeast,
PT plant or mammalian cells comprises altering ATP gradient across
XX biological membrane of target cell -

PS Claim 14; Page -: 85pp; English.

XX The present invention relates to a method for increasing or decreasing
CC drug resistance in target bacteria, yeast, plant or mammalian cells by
CC altering the ATP gradient across the biological membrane of the target
CC cell. The method is useful for modulating drug resistance of cells. It
CC is useful for increasing the sensitivity of cells to chemotherapeutic
CC and antibiotic agents and increasing resistance to herbicides. The
CC present sequence is from Pisum sativum and encodes an ecto-phosphatase
CC (extra-cellular phosphatase). This sequence was used in the present
CC Note: The present sequence is not shown in the specification, but is
CC referred to via its Genbank accession number.

XX Sequence 1661 BP; 501 A; 316 C; 310 G; 534 T; 0 other;

Query Match 56.4%; Score 839.8; DB 21; Length 1661;
Best Local Similarity 76.2%; Pred. No. 4,3e-229;
Matches 1062; Conservative 0; Mismatches 322; Indels 9; Gaps 2;

Qy 30 ttgagcaaaagcatgactcttcaatagtcacatgacctgtgtcaatgttaatgcc 89
Db 32 ttacactacaacaatgagctcctcttaacttaacttaccatttcttctatgc 91

Qy 90 tgcatactctctcccaatatctcgaaacacattctcaatgaatcgttaagatatct 149
Db 92 tgaatacactctctcccaatatcttaagaaacacattctcaatgaatgaatatttct 151
Qy 150 ccccaaaatcaggaacccagttacatcacaacgttgttataattgagtcgtgagcactg 209
Db 152 -----aaacaagagaattctctcttaagtcgtgagttatgagtcgtgagccgg 205
Qy 210 aagcagagtcacatgcttaacatttgatcagaacttaagttctctccgttgaacga 269
Db 206 tagtcgactacatgcttacaactttaaccagaacccagatcttctcatattggacaag 265
Qy 270 acttgatttattatgactcgtttaaccgcgttgaattgatacgcgtcactccctgaag 329
Db 266 tgttgatattataaataagaatacacacttggttgatctatacgcataataaccgaaga 325
Qy 330 agctgcagaatctctgattccacttcaaaagaagacagaanaatgtgtctcgtgaagca 389
Db 326 ggcgcgaataatctctcatccactttagagcaagcagaagatgtgtcccgacgatct 385
Qy 390 gcaaccacaacacccgttaagcttgaggcacaactgacgtttaaagctttgaggggaga 449
Db 386 tcaaccacaagaccccgtagacttgggcaactgcggtttaaggctttgaatggaga 445
Qy 450 tgcgtgaaatatalatgcaagcgttcagagatgctcagacacagaagtgccctaa 509
Db 446 tgccttgaaaaagatatgtaacttcgtaagagatatgctgcgacacagaagtaacttcaa 505
Qy 510 tgttcaatcagatgcagatcattcttgaattggaacccaagaagttcttacttgggt 569
Db 506 cgttcaaccagacgcagttctcataattgatgaaacccaagaagttcttactatggt 565
Qy 570 gacaattaaactctctcttggaagcttggaagaaagattcaaaagacgttggaggagt 629
Db 566 gacagttacatgcatctgaggaaatttaaggaaagaacacaaacagttggagtaat 625
Qy 630 tgactagaagtggtgcagtcgtaacatgacatgcagtcgaagacacacagctaaaa 689
Db 626 agactcttgagtgatcagtcacgttcaaatgagcgtatgagatcaaaagaacactgcataaa 685
Qy 690 tgcctcaaaagtaactgaaagagagatccatataaaagaagcttgaactccaaggaaa 749
Db 686 tgcctcaaaagttgagatgagagatgatacatatacaaaagaagttgaactcaaggaaat 745
Qy 750 gaaatagacctttagttcacagttacttgctgcatbgaagaagaagattgcgcgaga 809
Db 746 accataatgctcctatgttccacagttacttaacttcggttagagaagacatccgcagca 805
Qy 810 gatttcaagtcgcttggtgtgtctgctaalccttgcatatttagctgtgcttgaaggggc 869
Db 806 gatttgaagctcactctcctgctccctaaaccttgctttagtgatttaagat 865
Qy 870 atatacatatccgagacagagatataaagttctgcggcccaagcttaagatctaactgaa 929
Db 866 ctatacatattgaagagaagagtttaaggcaactcttcaactcttctgtgtcaaaatttaa 925
Qy 930 taaatgcgaagaagatagacttaagcgtcttaagaatgaatgacatttccatcaagaa 989
Db 926 taaatgcgaagaacaaatcgttaagcctttaaagttgaactatctctgtccatatacagaa 985
Qy 990 ttgcaactttgttgagatagaaatggtgagagtgtaagtggtcaaaaaaacttcttct 1049
Db 986 ttgcaactttgttgagatagaaatggtgagagtgtaagtggtcaaaaaaacttcttctg 1045
Qy 1050 tacttcaacttcttatacctctcgaagatggttgagatct---tgygaataaacccaa 1106
Db 1046 tcttcaacttcttcttatacctcgaagatgacggtatggttgaatgaaacacacctaa 1105
Qy 1107 tgcgaatctgctcagcttgatttgaagacgcacgaactaagcttgaataaacaact 1166
Db 1106 ttctactacttgcgcgcgcatatgagacaaagcttaaaagacttgcggttgaactt 1165
Qy 1167 tgaagatgcaaaatccaaatacccaagatcttattatgagaagacagtggttgaatatgtg 1226

Db 1163 cgagagatcggaatcctactatccattcttctgataagaaaatgtagcttcataatgta 1222
 QY 1227 cttagatcttgcttaactggtacacatgctgtgtgatagatttggtcttgatccattca 1286
 Db 1223 catgagcttctatacatgaatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1282
 QY 1287 agaggtacagtggtcgaaatgaatgaatcagatgctgtgtggaagccgcatggc 1346
 Db 1283 aaagattacatcaggaaggaagaaatgaatgaatcagatgctgtgtggaagccgcatggc 1342
 QY 1347 tctgagcaatgctcagatagaagaatcattatcattatgcttaattgagagatgaattat 1406
 Db 1343 tctagcaatgctgtagaagcatalcagcttaccctaaattgagcgattgattat 1402
 QY 1407 tatttaactact 1419
 Db 1403 tgttaagttctc 1415

RESULT 5

AAF85680
 ID AAF85680 standard; DNA; 1697 BP.

AAF85680;

25-JUN-2001 (first entry)

Pea blight resistance protein coding sequence #2.

Pea; blight resistance; nucleotide triphosphate decomposition; ds.

Pisum sativum.

Key Location/Qualifiers

FT CDS 25..1392

FT /tag= a /product= "Blight resistance protein"

PN JP2001017176-A.

PD 23-JAN-2001.

PF 02-JUL-1999; 99JP-0189129.

PR 02-JUL-1999; 99JP-0189129.

PA (KYOU) UNIV KYOTO.

DR WPI: 2001-320697/34.

DR P-PSDB; AAB81952.

PT New blight-resistant polypeptide useful for giving blight resistance to

PS a plant -

XX Claim 4; Page 12-13; 20pp; Japanese.

CC The present invention provides the protein and coding sequences of a

CC pea protein with nucleotide triphosphate decomposing activity. The gene

CC sequence is one version of the coding sequence of the invention.

XX Sequence 1697 BP; 535 A; 308 C; 306 G; 548 T; 0 other;

Query Match 56.0%; Score 833.4; DB 22; Length 1697;

Best Local Similarity 76.0%; Pred. No. 2.9e-227;

Matches 1058; Conservative 0; Mismatches 326; Indels 9; Gaps 2;

QY 30 ttgagcaaatgctgacttcttaattagctcagatgacttggttcatgtaagcc 89

Db 12 ttacctacaacaatgagtgcttacttaactatcacttttctactattttctatgc 71

QY 90 tgcattctctccccaatctctgaaacacacattctcattgaatcgttaagattact 149
 Db 72 tgcataactctccccaactactagaaacacactactaccagatagaagaatttctc 131
 QY 150 ccccaaaaacagaaacacatcatcatcgcgtgtatatttgatgctgtgtagcactg 209
 Db 132 -----aaacaagagagaatttcccttaagctgtatgattatgcgcgtgtagcactg 185
 QY 210 aagcagatcactgctacaaattttatcagaacttagatcctccgttgaagaaga 269
 Db 186 tagtcgactatcaatgaatcattttaaccagaacttagaccttctcatattgycaaag 245
 QY 270 acttggtttatgattgctgtaaccggttgattgaattatgcgcgtcattcctgaaga 329
 Db 246 tgcgagatataataaagaatacaccgtgtgtgagttcattagcgtcaataatccagaaga 305
 QY 330 agctgcaaatctctgattccacttcaaaagaagacagaanaatgltgtctcgtgagca 389
 Db 306 gctgcaaaaatctctcatccacttttagagcaagacagaagatgctgtcccgagactc 365
 QY 390 gcaacccaacacacccgttaagcttggtgcaactgcaggtttaaagctttgagggaga 449
 Db 366 tcaacccaagacacccgttagacttgggcaactgcccgtttaaagctttgaaatgaga 425
 QY 450 tgcgtgtaaaaataatgcaagcggtcagggatagctcagcaagaagtgcccttaa 509
 Db 426 tgccttgaagaagatattgcaatcgtaagagatattgctgagcaagaagatccttcaa 485
 QY 510 tgtcaatcagatgcatctatcttcttgatggaacccaagaagttcttactttggt 569
 Db 486 cgtcaacccaagcagcttctataattgatggaacccaagaagttcttactatggt 545
 QY 570 gacaattaactatctcttggtggaagttggaagaagattcaagaagcgtgagtagt 629
 Db 546 gacaattaaactatgcatggaatttaaggaaagatcaacaaaacggttggat 605
 QY 630 tgatcagaagtggtgctgcaaatgacatgcagctcagctcaagaacacagcaaaa 689
 Db 606 agacttggaagtgatcagctcaatggtcgaatggtcagatgatacaaaaacgtcgaaaa 665
 QY 690 tgcctcaaaagttaactgaaggaagatcatalcaataaagaagcttgaactcaaggaa 749
 Db 666 tgcctcaaaagttaactgaaggaagatcatalcaataaagaagcttgaactcaaggaa 725
 QY 750 gaatatgacctttagttcacagttacttgcgtatggaagaagaagattcgtgcaga 809
 Db 726 accatatgactttagttcacagttacttgcgtatggaagaagaagattcgtgcaga 785
 QY 810 gatttcaagtcgctggtgtgtctgctaalccttgcatatttagctgcttgaaggagc 869
 Db 786 gatttgaagtcacactcctgctcccttaaccccttgctttagctgatttaagtaag 845
 QY 870 atatacatattccgagcagagataaaggtcgtgcgccccagcttgaagatcactaa 929
 Db 846 ctatacatattcagaggaagaatttaaggcaactgtcttaccacttgtgtgcaaaacttaa 905
 QY 930 tcaatgcagaagaatagactcttaagccttaagaatggaatgacacttgcctatcaga 989
 Db 906 taaatgcagaagaatcagactgtgaagccttaagaatggaatgacacttgcctatcaga 965
 QY 990 ttgcaacttgggtgataatggaatggtggaagtggaagtggtgcaaaaacttctcct 1049
 Db 966 ttgcaacttgggtgataatggaatggtggaagtggaagtggtgcaaaaacttctcct 1025
 QY 1050 tactcatcttcttacttaccctctgaaagatgttggagctc---tgtgaataacccaa 1106
 Db 1026 ttctcatcttcttcttaccctcgaagataccggtatggttgaatgacaacaccta 1085
 QY 1107 tgcgaatctgctcagacttgaatggaagcgcgaactgaactggttgaataaactct 1166
 Db 1086 ttctcatcttggcgcgtcagatattgagactaaagctaaagaagcttgcgcgttaactc 1145
 QY 1167 tgaagatgcaaaaatccaaatacccaagatcttattgagaagaagacagtggttgaata 1226

Db 1146 cgaggatgcgaatacttacttacttctctgataagaanaatgtagcttcatatgatatg 1205
Oy 1227 ctgtgactctgtctacgtgtacacatgctgtgtgtatgtgattgtgtcttgatccatcca 1286
Db 1206 catgactcttatatactcagatgtgtactcgtgtatgtgattgtgtcttgatccatcca 1265
Oy 1287 agaggttaccgtgtgcgaatggaatggaatcatcagatgtgtctgtgtggaagccgcatgccc 1346
Db 1266 aaagattacatcagaaggaatggaatggaatcagaatgctgtatgtgtggaagcgtgcatgccc 1325
Oy 1347 tctagacactgtgcgaatggaatggaatcagaatgctgtatgtgtggaagcgtgcatgccc 1406
Db 1326 tctagacactgtgtgtggaaggaatcagaatgctgtatgtgtggaagcgtgcatgccc 1385
Oy 1407 tatttaactact 1419
Db 1386 tgttaagtctct 1398

RESULT 6

AAF85679
ID AAF85679 standard; DNA; 1368 BP.

AAF85679;

25-JUN-2001 (first entry)

Pea blight resistance protein coding sequence #1.

Pea: blight resistance; nucleotide triphosphate decomposition; ds.

Pisum sativum.

Key Location/Qualifiers

FT CDS 1..1368

/*tag= a /product= "blight resistance protein"

JP2001017176-A.

23-JAN-2001.

02-JUL-1999; 99JP-0189129.

02-JUL-1999; 99JP-0189129.

(KYOU) UNIV KYOTO.

WPI: 2001-320697/34.

P-PSDB; AAB81952.

New blight-resistant polypeptide useful for giving blight resistance to a plant -

Claim 3; Page 12; 20pp; Japanese.

The present invention provides the protein and coding sequences of a pea protein with nucleotide triphosphate decomposing activity. The gene can be used for conferring blight resistance on a plant. The present sequence is one version of the coding sequence of the invention.

Sequence 1368 BP; 422 A; 260 C; 275 G; 411 T; 0 other;

Query Match 55.8%; Score 830.4; DB 22; Length 1368;

Best Local Similarity 76.3%; Pred. No. 1.9e-226;

Matches 1049; Conservative 0; Mismatches 316; Indels 9; Gaps 2;

Oy 43 atgagcttcttaattagctatgacacctgtgttcatgttaatgctgtatctcttc 102
Db 1 atggagcttcttaattagctatgacacctgtgttcatgttaatgctgtatctcttc 60

Oy 103 tcccaatactcggaaacacacattctcatgtaactgtaagataatactccccaataatcag 162
Db 61 tcccaatactcggaaacacacattctcatgtaactgtaagataatactccccaataatcag 114
Oy 163 gaacaggttacatcactgctgtatatttgatgtgtgtgtagcactgtgaagcagagtcact 222
Db 115 gaggaaattctcttactgactgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 174
Oy 223 gctcaaatctgtatcagaacttgaatctctccctgtgtgaagaaagaaactgtgtgtgt 282
Db 175 gttaccattttaaaccagaacttgaacttctcatattgtgaagagtgctgagatattat 234
Oy 283 gattcggttaaacccggtttgagttgatacgtgtgtaactcctggaagaaactgcaagatc 342
Db 235 aataagataacacccggtttgagttgatacgtgtgtaactcctggaagaaactgcaagatc 294
Oy 343 ctgattccactcttaaaaagacagaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 402
Db 295 ctcatccactttagagagcagaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 354
Oy 403 ccggttaagctgt 462
Db 355 ccggttaagctgt 414
Oy 463 atattgcaagcgt 522
Db 415 atattgcaagcgt 474
Oy 523 gcaatctctatctgt 582
Db 475 gcaatctctatctgt 534
Oy 583 cctctgt 642
Db 535 gcaatctctatctgt 594
Oy 643 ggttcagtgcaatgacatgacatgacatgacatgacatgacatgacatgacatgacatgac 702
Db 595 ggttcagtgcaatgacatgacatgacatgacatgacatgacatgacatgacatgacatgac 654
Oy 703 cctgaagagagagatccatcacaataaagaagctgtgtgtgtgtgtgtgtgtgtgtgtgt 762
Db 655 gcatgt 714
Oy 763 tatgttcacagttactgt 822
Db 715 tatgttcacagttactgt 774
Oy 823 gctgt 882
Db 775 actcctcgttctccttaacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 834
Oy 883 ggaagcagatataaggt 942
Db 835 ggaagcagatataaggt 894
Oy 943 atagcttcaaggt 1002
Db 895 acaatcgttaaggt 954
Oy 1003 gggataatgaggt 1062
Db 955 ggaatctgtgaatgt 1014
Oy 1063 tattaactctgtgaatgt 1119
Db 1015 ttttaactcctcgaagatacggatgt 1074
Oy 1120 ccagttgatttgaagactgt 1179
Db 1075 ccggttcagatgt 1134
Oy 1180 tccaaataccagatcttattgagaagaacagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1239

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Db 1135 tctactatccattctctgataagaataatgtagcttccatctatgtacatgtagctctata 1194
Oy 1240 taegttacacattgcttgtttgtagtaattggtcttgatccattcaagaagatcaagtg 1299
Db 1195 taccagtaatgttactcgttctgtatgtattggtcttgatccattcaagaagatcaatca 1254
Oy 1300 gagaagaattgaatcaatcaatgagatgctctgtgagagccgcatgagcctctagagcactg 1359
Db 1255 gggaaaggaattggaataccaagatgctatgttggaaagccgcatgagcctctagagcactg 1314
Oy 1360 atagaagcaatcatcatcatgctcctaaattgagagataatgattattttaa 1413
Db 1315 gtagaagcaatcatcatcatgctcctaaattgagagatgattattttaa 1368

RESULT 7
AA08522
ID AAX08522 standard; cDNA; 1643 BP.
AC AAX08522;
XX
XX 19-JUL-1999 (first entry)
DE NBP46 (root lectin) cDNA.
XX
XX NBP46; Lectin; Rhizobium; leguminous plant; transgenic plant;
KM nitrogen; nitrogen fixation; fertilizer; ss.
XX
XX Dolichos biflorus.
XX
XX
XX Key Location/Qualifiers
XX CDS 51..1439
XX FT /tag= a
XX FT /product= "NBP46 (root lectin)"
XX
XX WO9907223-A1.
XX
XX PD 18-FEB-1999.
XX
XX 05-AUG-1998; 98WO-US16261.
XX
XX 06-AUG-1997; 97US-0907226.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX PA
XX PI Etzler ME, Murphy JB;
XX
XX WPI; 1999-167136/14.
XX DR P-PSDB; AAM85684.
XX
XX
XX New polynucleotides encoding Nod factor binding lectins - useful
XX PT for production of transgenic plants which are able to fix nitrogen
XX
XX PS Claim 3; Page 42; 57pp; English.
XX
XX The NBP46 root lectin is instrumental in recognising and binding
XX CC to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate
XX CC interaction. The production of transgenic plants comprising an
XX CC expression cassette expressing the NBP46 root lectin is advantageous
XX CC since it would mean that non-leguminous plants could fix nitrogen
XX CC from the atmosphere, lessening the need for the addition of nitrogen
XX CC containing fertilizer to soil. This would lead to higher crop yields
XX CC where soil has been overplanted and replenishment of the depleted
XX CC soil with usable nitrogen. Alternatively, expression of NBP46 can be
XX CC used to modulate oligosaccharide signalling in the plant. The nucleic
XX CC acid sequences can be used to inhibit expression of an endogenous
XX CC gene and also to suppress endogenous NBP46 gene expression.
XX
XX Sequence 1643 BP; 505 A; 317 C; 347 G; 474 T; 0 other;

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Query Match

55.4%; Score 824.6; DB 20; Length 1643;

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Best Local Similarity 76.7%; Pred. No. 9,4e-225;
Matches 1049; Conservative 0; Mismatches 309; Indels 9; Gaps 3;

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Db 86 ctctccactctccatctactcttctactcttccatctgaacaaacttcttcgcaata 145
Oy 111 tctcgaaacaacattccatctgatctgaatattcccccacaataacagaacagt 170
Db 146 tgttgggaacagatattcttaataatcatctgaataacttccaaac---caggaaactct 202
Oy 171 taacataacgctgtataattgagtcgttagcacatggaagcaagatccatgttcaaa 230
Db 203 taaccttaagctgtcatcttgatgtctgtagctctggagtcgtccatgtcttcaa 262
Oy 231 ttgttgcgaacttgatctctctccgttgaaacagcaacttgattatgattcgt 290
Db 263 ttctgaccgaacttgatctctccgtgacatggaacatccctgagattcaaaaaaagat 322
Oy 291 taaccggtttgagttcatagctgtctaatcctgagaagatgacgaatctctgtatcc 350
Db 323 caaacccggtttgagttcatagctgtataagcttgaaaaagctgcaagaatctctatcc 382
Oy 351 acttcaaaagaagcagaataatgtgttctctgtgagccagcaaccacacaccgttaa 410
Db 383 actttggaggaagcgtgaagatgtgttccctgagaaactgcaccccaagacacccttaa 442
Oy 411 gcttgggcaactgcaggttttaagcttttggagggaatgtcgtcgtaaatatattga 470
Db 443 gcttgggcaacagcaggtttgagctcttgatgttgaggtcgtcgtaaaaatatttga 502
Oy 471 agcggtaaggatctgctacagcaacagaagtgcccttaattgttcaatcagaagcagatc 530
Db 503 agcggtaaggatctgctacagcaacagaagtgccctgagcgttcaacccgtagcagatc 562
Oy 531 taattcttgaggaacccaagaaggttctatcttgggtgacaaatataactatctctgg 590
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Oy 951 taaggtcttaagaatgtaacactgttccatccatcagaattgaacttgggtggagatg 1010
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Oy 1011 gaatgtgtgaggtgtaagatgtgtcaaaaaaacttcttctaacttaacttctbataact 1070
Db 1043 ggaatgtgtgaaaggaagtggaacagaanaaactgtgttacttccagcttctactatag 1102
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Db 1005 tggcggtggtgagctggggaaacaacttttggatcattcttcttgaagtgyc 1064
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QY 1131 gaagactgcagctaaatagcttcttgaataacaatctgagatccaataccccc 1190
Db 1125 tgaagatgcagcaaggttcttcttcttgaatccaagatccaatccgtttccc 1184
QY 1191 agactcttgaagaagaacagctgttgaatatgtgtcttggatcttctcagtgtcac 1250
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QY 1251 atgtctgttgaatgattgtcttgaatccattccaagaagttacagtgccaatgaaat 1310
Db 1242 atgtctgttgaatgattgttgcattgtccccaagaagattacattgttgaagcaat 1301
QY 1311 tgaatataagatgctcttcttgaagccgcatgtgcctctagcactgcataagaagcaat 1370
Db 1302 tcaatataagatgattctcttcttgaagctgcattgcacactgcagaagtgcataagaagcaat 1361
QY 1371 atcatcttgcctaaatttgaagataatgtatttatttaact 1416
Db 1362 atcttcttaccctaaatttgaagaattatgtatttcttcttgaagct 1407
RESULT 9
AAC39492
ID AAC39492 standard; DNA; 1981 BP.
XX
AC AAC39492;
XX
DT 17-OCT-2000 (First entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24831.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.

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PR 22-OCT-1999; 99US-0160989.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 30.3%; Score 451.6; DB 21; Length 1981;

Best Local Similarity 63.3%; Pred. No. 2,6e-118;

Matches 763; Conservative 0; Mismatches 423; Indels 14; Gaps 4;

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OY 178 tacgtgtatatttgatctgtgtagcactggaagcagatccatgctacatttgat 237
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DB 502 tacgtgtattttgtagctggaagttctggaagcgtgtagctgttactgttcgat 561
OY 238 cagaacttagatctccctccgtgtaaaacgaacttgattttagatcggttaacc 297
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DB 562 cagaatttgatctgtctctcttggaatgagctcgaagctctcttaacgaataaacg 621
OY 298 ggttgatctacagctgctaatccctgaagagctgcagaatcctgattccactcta 357
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DB 622 ggttaagtgcatacccaatgatctcctgcgaacacgaactctttagtaactcttcg 681
OY 358 aagaagcagaaatggtgttcctgtgagccagcaaacacacacccgtaagcttgag 417
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DB 682 gacaagcagaagctccgtccctccgtgagctgcgtcccaagaactcctgcagagttg 741
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DB 742 gcaactgaggtttgagagcttttggtgcaacagcctcgaaaacttgcgaagc---- 797
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OY 538 gatggaaccacaagagtgcttctatcctttggtggaatattactctcttgggaagtgc 597
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DB 1217 gctgcagcttccatcccggtgcaagcttagatgtagtgcggcgagtagcttataagca 1276
OY 958 cttaagct---gaatgcacctgtccctacgaatcttgacctttggtggatgaagt 1014
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Db 3239 aggt 3242

RESULT 12

ID AAF63402 standard; DNA; 1287 BP.

AA63402;

14-MAY-2001 (first entry)

Human CD39 like protein CD39-L4 coding sequence.

Human CD39-like protein; apyrase; ND Pase; platelet function inhibitor;
myocardial infarction; cerebral ischemia; angina; arterial thrombosis;
cerebral artery thrombosis; platelet aggregation; inflammation;
apoptosis; autoimmune disorder; neurological disorder;
Alzheimer's disease; Parkinson's disease; cancer; CD39-L4; ds.

Homo sapiens.

WO200110205-A1.

15-FEB-2001.

09-AUG-2000; 2000WO-US21790.

09-AUG-1999; 99US-0370265.

11-JAN-2000; 2000US-0481238.

25-APR-2000; 2000US-0557800.

26-MAY-2000; 2000US-0583231.

30-JUN-2000; 2000US-0608285.

(HYSE-) HYSEQ INC.

Ford J, Mulero JJ, Yeung G;

WPI; 2001-147489/15.

P-PSDB; AAB72243.

Disclosure: Page 140-142; 203pp; English.

This invention relates to polynucleotides encoding human CD39-L4-like polypeptides with apyrase and/or ND Pase activity. The polypeptides having apyrase, including ND Pase, activity are useful for inhibiting platelet function and can therefore be used in the prophylaxis or treatment of pathological conditions caused by or involving thrombosis or excessive coagulation or excessive platelet aggregation, such as myocardial infarction, cerebral ischemia, angina, arterial thrombosis, cerebral artery thrombosis or intracardiac thrombosis, and conditions associated with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in modulating disease states (including platelet aggregation, inflammation and apoptosis) associated with ADP or other purinergic signalling by reducing the levels of NDPS. The polypeptides are also useful for prophylaxis or treatment of inflammation related disorders, such as disorders involving sepsis or systemic inflammatory response syndrome or SIRS (and associated conditions such as fever, tachycardia, tachypnea, cytokine overstimulation); autoimmune disorders such as thrombosis, atherosclerosis, acute pancreatitis, dermatitis, including psoriasis, cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis; neurological disorders including neurodegenerative diseases, epilepsy, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis; and cancer. The present sequence represents the CD39 like protein CD39-L4 coding sequence.

Sequence 1287 BP; 330 A; 290 C; 344 G; 323 T; 0 other;

Query Match 6.1%; Score 91.2; DB 22; Length 1287;
Best Local Similarity 50.0%; Pred. No. 14e-15;
Matches 256; Conservative 0; Mismatches 253; Indels 3; Gaps 1;

QY 150 ccccaaaatcagaacccgttaccatcatcagctgtatatttgatgctgtgtagcctg 209

Db 117 ccccatcatgttcagcgcgcagccactctgtatgaattatgttgatgcaggagcactgg 176

QY 210 aagcagatcatcgtctacaatttgcagaactagatctctccgttgaaacga 269

Db 177 aactcgatcatcgttacaactttgtcagaanaatgcagcagcttccaattcaga 236

QY 270 acttggtttatgatctggttaaccggtttgagttcagttcagctcgaatcctga 329

Db 237 agggagagttttgatctcgtgagccaggaactctgtctttgtatgaactaagca 296

QY 330 agctgagaaatctctgattccacttctaagaagaagaatgtgtctgtgagcca 389

Db 297 ggggtgtagagaccgttcaagggctcttagaggtggtccaaagactcaatccccgaagta 356

QY 390 gcaaccacaacaccgttaagcttggggaactgcaggttaagctttggagggaa 449

Db 357 ctggaanaaagaccctcagtggttctaaggaacagcaggaactcagcttaccagaaca 416

QY 450 tgcgtgaaatataattgcaagcgtcaggaatgctcagcaacagaagtgcccttaa 509

Db 417 caaagccaaagcctcgtctctttaggttaaggaatccttaggaagcacttctc 473

QY 510 tgttcaatcagatgcagatctatcttcttgatggaaccagaagaagttctatttgggt 569

Db 474 gttcaacaagggcagtgtagcatcagatgtagtgcgacgaaggaatataagcttgggt 533

QY 570 gacaatcaactatctcttggggaagttgggaattcaacaagaacagtcggagtagt 629

Db 534 tactgtgaattcttcgacaggtcagctcagtcagccaaagcaggaagacgttgggagcctt 593

QY 630 tgatctagagagtggttcagtgcaatgacat 661

Db 594 ggaactagggggagccctccacccaatcagct 625

RESULT 13

AAZ50358

AAZ50358; standard; CDNA; 1601 BP.

18-MAY-2000 (first entry)

Human CD39-L66 protein encoding cDNA.

CD39-L4; human; CD39-L66; apyrase; nucleotide diphosphatase; ND Pase;
ADP diphosphohydrolase; Apyrase; adenosine diphosphate; ADP; treatment;
platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
cerebral ischemia; angina; vascular graft; extracorporeal circulation;
molecular weight marker; nutritional supplement; tumour; prevention;
drug targeting; splice variant; ss.

Homo sapiens.

Location/Qualifiers

Key 246..1463

CD3 /tag- a "Human CD39-L66 protein"

WO200004041-A2.

27-JAN-2000.

16-JUL-1999; 99WO-US16180.

PR 16-JUL-1998; 98US-0118205.
 PR 24-JUL-1998; 98US-0122449.
 PR 04-FEB-1999; 99US-0244444.
 PR 19-MAR-1999; 99US-0273447.
 PR 09-JUL-1999; 99US-0350836.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Ford J, Mulero J;
 XX
 DR WPI: 2000-182397/16.
 DR P-PSDB: AAF44851.
 XX
 PR New nucleic acid encoding human CD39-like protein, useful for treating
 PI and preventing thrombotic disease -
 XX
 PS Claim 8; Page 123; 125pp; English.
 XX
 CC The present sequence is a cDNA encoding the CD39-like protein, a splice
 CC variant of CD39-L4 protein. It is an apyrase and/or nucleotide
 CC diphosphatase (NDPase), isolated from the human foetal liver-spleen cDNA
 CC library, b2HFLS20W. It is a soluble ATP diphosphohydrolases (ATPase) and
 CC is involved in the hydrolysis of adenosine diphosphate (ADP), the agonist
 CC that causes platelet aggregation. CD39-L4 protein has 30% and 80%
 CC homology to human and murine CD39. It has platelet aggregation inhibition
 CC and antithrombotic activity. CD39-L4 is used to treat or prevent
 CC thrombosis, myocardial infarction, cerebral ischaemia and angina. It is
 CC also used in vitro, to maintain vascular grafts or during extracorporeal
 CC circulation, to hydrolyse NDP, as molecular weight markers and as
 CC nutritional supplements. It is used to identify therapeutic agents that
 CC bind and modulate CD39-L4. It is coupled to toxins for targeting drugs
 CC to tumours or other cells that express CD39-L4.
 XX
 SO Sequence 1601 BP; 436 A; 352 C; 428 G; 385 T; 0 other;

Query Match 6.1%; Score 91.2; DB 21; Length 1601;
 Best Local Similarity 50.0%; Pred. No. 1.5e-15;
 Matches 256; Conservative 0; Mismatches 253; Indels 3; Gaps 1;

QY 150 ccccaaaatcaggaaccaggtatcatcatcagctgttatatttgctgtagacactg 209
 DB 362 ccccatcatgctcagcgacgacactgtatgtaattgttgtagcgaggacactg 421
 QY 210 aagcagagtcctatgctcaatttgcagaacttagctccctccgttgaaacga 269
 DB 422 aactcgaattcatgttacccttctgtagcaaaaatgcagacagcttccaattctaga 481
 QY 270 acttgagtttatgattcgtttaaacccggttgagttcatagcgtctcatcctgaaga 329
 DB 482 aggggaagtttattgattcgtgaagcaggaacttctgtttttagatcaactaaga 541
 QY 330 agctcagaatctctgattcacttctaaagaagcaaaaatgtgtctctgttgaca 389
 DB 542 gggctcgtgacgcttcaagggtcttagagtgtagcaagctcaatcccccgaagta 601
 QY 390 gcaaccacaacaccggttaagcttggtgcaactgcaggttcaagcttcttgaggaga 449
 DB 602 ctggaaaaagaccagctgtgtcttaaggaacacagacgacttctcccaaga 661
 QY 450 tgcctcgtgaataatattcgaagcgttcaggaatgctgcacgaacagagtgccctta 509
 DB 662 caaagcgaagctcgtctcttggagtaagaagatcttcaaggaagctccttctct 718
 QY 510 tcttaacatcagatgcatatctattcttgatggaaccagaaggtcttattcttgggt 569
 DB 719 ggtaccagaagggcaggttagcatcatgtagatcgcgaggaagatattgacttgggt 778
 QY 570 gacaattactatctcttggggaaggttggaaaaattaccagaacagctgggaatgt 629
 DB 779 tactgtgaatttctgtacagcttcatgtgacatgtagccacagacagagactctgggagactt 838
 QY 630 tgatctagaggtgtgtagtgcgaatgacat 661

DB 839 ggacttagggggagcctccaccacaatacactg 870
 || ||||| || || ||||| || ||
 RESULT 14
 ID AAF63384
 AC AAF63384 standard; cDNA; 1601 BP.
 XX
 AC AAF63384;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Human cDNA encoding CD39 like protein CD39-L4.
 XX
 KW Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
 KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
 KW cerebral artery thrombosis; platelet aggregation; inflammation;
 KW apoptosis; autoimmune disorder; neurological disorder;
 KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4; sg.
 XX
 OS Homo sapiens.
 XX
 PN WO200110205-A1.
 XX
 PD 15-FEB-2001.
 XX
 PF 09-AUG-2000; 2000WO-US21790.
 XX
 PR 09-AUG-1999; 99US-0370265.
 PR 11-JAN-2000; 2000US-0481238.
 PR 25-APR-2000; 2000US-0557800.
 PR 26-MAY-2000; 2000US-0583231.
 PR 30-JUN-2000; 2000US-0608285.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Ford J, Mulero JJ, Yeung G;
 XX
 DR WPI: 2001-147489/15.
 DR P-PSDB: AAF72239.
 XX
 PT Polynucleotides encoding human CD39-like polypeptides, with apyrase
 PT and/or NDPase activity, which are useful in the treatment of
 PT pathological conditions caused by thrombosis (e.g. myocardial
 PT infarction) and inflammatory disorders -
 XX
 PS Claim 10; Page 156-157; 203pp; English.
 XX
 CC This invention relates to polynucleotides encoding human CD39-like
 CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
 CC Arpase, including NDPase, activity are useful for inhibiting platelet
 CC function and can therefore be used in the prophylaxis or treatment of
 CC pathological conditions caused by or involving thrombosis or excessive
 CC coagulation or excessive platelet aggregation, such as myocardial
 CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
 CC artery thrombosis or intracardiac thrombosis, and conditions associated
 CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
 CC modulating disease states (including platelet aggregation, inflammation
 CC and apoptosis) associated with ADP or other purinergic signalling by
 CC reducing the levels of NDPs. The polypeptides are also useful for
 CC prophylaxis or treatment of inflammation related disorders, such as
 CC disorders involving sepsis or systemic inflammatory response syndrome or
 CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
 CC cytokine overstimulation); autoimmune disorders such as thrombosis,
 CC atherosclerosis, acute pancreatitis, dermatitis. Including psoriasis,
 CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
 CC neurological disorders including neurodegenerative diseases, epilepsy,
 CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, and amyotrophic lateral sclerosis; and cancer. The present
 CC sequence represents cDNA encoding CD39 like protein CD39-L4.
 XX
 SO Sequence 1601 BP; 436 A; 352 C; 428 G; 385 T; 0 other;

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Db 618 gaagccagctctgctcttgagtagagagatcttcaagaattcccttctct--- 674
QY 510 ttttaataagatgagatctatcttcttgatgaaaccaagaagttcttactttgggt 569
Db 675 ggtcccaagatgagcagcttagatcatgagtggtcctctatgaaagcalactagctgggt 734
QY 570 gacattactctctcttgagggaattgggaaagatttacaagacagtgaggagtgct 629
Db 735 taacgtgaactcttcttcaaacagtgatgctgctgctgagagagactgtggagacct 794
QY 630 tgatctagaggtggtgagtgacatgacatat 663
Db 795 tgacctgggggtgctctccacccaataacagcttt 828

RESULT 2
US-09-608-285A-4
Sequence 4, Application US/09608285A
Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608, 285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583, 231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557, 800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481, 238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370, 265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350, 836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273, 447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244, 444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122, 449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118, 205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 4
LENGTH: 1287
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1284)
US-09-608-285A-4

Query Match 6.1%; Score 91.2; DB 4; Length 1287;
Best Local Similarity 50.0%; Pred. No.1.5e-18;
Matches 256; Conservative 0; Mismatches 253; Indels 3; Gaps 1;

QY 150 ccccaaaaatcaggaacagttacatcatcagctgtatataattgagtgtgtagcactg 209
Db 117 ccccatcaatgctcagcgacgacactgtatgtaattatgttgatgagggagcgactg 176
QY 210 aagcagagtcacatgcttaacaatttgatcagaacttagatctctccctccgttgaaga 269
Db 177 aactcgaatcactgtttacaccttgtgcagaaatgccagcagcttcccaattctaga 236
QY 270 acttgagttatgatctcggttaaacccggttgtagttcctaagctgctaactctgaaga 329

Db 237 aggggaagtttttgattctgtgaagccagagacttctgcttttgtagatcaactaagca 296
QY 330 agctgcgaactctctgtattccacttcttcaaaagaagcagaatattgtttctgtgagca 389
Db 297 ggggtgttgaagccgtlcaaaaggtccttagagtggtgcacaagactcaatccccagtlca 356
QY 390 gcaaccacacacaccggttaagcttggtggaactgcaggttttaagcttttgagggaa 449
Db 357 ctggaanaagagccccagtggtcctcaaaagcacaagcagactaagcttaactgccaagaa 416
QY 450 tgcgtcgaataatatttgcaagcgtcagggatagatgctcagaacaagagtgcccttaa 509
Db 417 caagccaagctctgctcttgtagtaagaagatctcagaagcacccttctct--- 473
QY 510 tgtcaatcagatgacatctatcttcttgatgaaaccaagaagttcttactttgggt 569
Db 474 gttaccaagggcagtggttgacatcagatgagtcctgcagcagagcatattagcttgggt 533
QY 570 gacattactatctcttgagggaagttgggaaaaagatttacaagacagtgaggagtagt 629
Db 534 tactgtgaattttctgacaggtcagctgcagtcagacagcagagagactgtgggacctt 593
QY 630 tgatctagaggtggtcagtgcaatgacat 661
Db 594 ggaactaggggagcctccacccaataacagct 625

RESULT 3
US-09-608-285A-24
Sequence 24, Application US/09608285A
Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608, 285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583, 231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557, 800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481, 238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370, 265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350, 836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273, 447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244, 444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122, 449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118, 205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 24
LENGTH: 1601
TYPE: DNA
ORGANISM: Homo sapiens
US-09-608-285A-24

Query Match 6.1%; Score 91.2; DB 4; Length 1601;
Best Local Similarity 50.0%; Pred. No.1.7e-18;
Matches 256; Conservative 0; Mismatches 253; Indels 3; Gaps 1;

QY	150	ccccaaaatacgaagaaacacagttacatcatcgcgtgtatatatttgatgctgtgtagcacctgg	209
Db	362	ccccatacaatctcgcgcgcgcacgaacctgttatgtgatattatgttatgttcaggagacactgg	421
QY	210	aagcagaatccatctatctacaattcttgatccgaacttgaatcttcctcccttgtaaaacga	269
Db	422	aactcgaaattcatigtatttaacaccttcttgccagaaaatgcccagacagcttccaatctctaga	481
QY	270	acttgagtttataatgattccggtttaaacccggtttgtagttcatcagctgtgtaacctggaaga	329
Db	482	aggggaagttttttgatctcttgaaagccaggaactcttcgctctttgtgatcaactaaagca	541
QY	330	agctcgagaatccttgattccacactctccaagaagaagcagaanaatggtgttcctgtggcca	389
Db	542	gggtgctcgagagccggttcaagggctcttaagggtggtggccaaagaacttcaatccccgaagtca	601
QY	390	gcaaccccaacacacaccggttlaagctcttggtggcgaactgcaggtttaaggcttttggaggga	449
Db	602	ctggaaaaaagcccccaatgtgtctctaaagggaacacgcgcgactcgaactatgcacagaaca	661
QY	450	tgctgcctgaaataatattgtgcagaagcgtgcagggatctcatgatacgaacaagaagtgccttaa	509
Db	662	caaaagccaaagctctgcctcttcttgtaggtggttaaaaggatcttcaaggaaagtcaacttccc---	718
QY	510	tgttccaatcagaatgcagatcatctattcttgaatggaaccacaagaaggtcttatcttttgggt	569
Db	719	ggtcccaaaagcgagtglttgatcatcatgatatgataccgacgaagcatattagctcttgggt	778
QY	570	gacaaattacatcatctcttggtggaagtgtggaaaaaagtttaacaaagaacatggagtagt	629
Db	779	tactgtgaatttcttgacaaagttcagctgcgcataatgcacagaacagaaggaactgtgggaacct	838
QY	630	tgatctagaggtggtgtcaagtgcgaatgacat	661
Db	839	ggaccttaggggaagcctccacccaataatcacagt	870

RESULT 4
US-09-608-285A-2
; Sequence 2, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/563,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 2
;
; LENGTH: 1799
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: CDS
;
; LOCATION: (246)..(1529)
;
; NAME/KEY: misc feature
;
; LOCATION: (1718)
;
; OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
;
; OS-09-608-285A-2

```

Query Match	6.1%;	Score 91.2;	DB 4;	Length 1799;
Best Local Similarity	50.0%;	Pred. No. 1.9e-18;		
Matches 256;	Conservative 0;	Mismatches 253;	Indels 3;	Gaps 1.

OY	150	ccccaaaaatacgaagaccagttacatcatacagctcgttatatttgatgctgtgtagcactg	209
Db	362	ccccctcaatcattcgagcgccagccacaccttgatgatgaattatgttatgacagggagcactgg	421
OY	210	aagcagaatcccatgatctcaaatctttgatacgaactctgatctccctccgttgaaaaaga	269
Db	422	aactcgatattcatgttttaacaccttggcaggaataatgcagacagcttccaattccaga	481
OY	270	acttgagtttattgaattccgtgttaaacccggtttgagttacatagctcgtctaatccctgaaga	329
Db	482	aggggagaatttttgaattcttgtaagcagcagacttcctgcgttttgtaatatcaactaagca	541
OY	330	agctgcagaatcctcgtgatctcaactctcaaaaagaacagagaatgtggttccttgtaacca	389
Db	542	gggtgctgtagcgcgttcaaggcgtctctatgaggtggtccaaagatccaatcccccgaagtca	601
OY	330	gcaaccccaacacaccocgtttaagctcttggtggcgaactgcaggttttaagcttttgaaaggga	449
Db	602	ctggaaaaaagccccagctggtctctaaaggccaacagcagactgaagcttaattgcagaagaca	661
OY	450	tgctcgtcaaaaatatatctgcagaagcgtgtcgaagatactgcacagacagaagtgcccttaa	509
Db	662	caaaagccaagctctcgcgtcttcttggtgtaaaagagatacttcaaggaagcaccttccct---	718
OY	510	tgttcaatcagatgcagatcatctattcttgatggaacccaagaaggtctctatcttgggt	569
Db	719	ggtaccaaagagcaggtgttgatgacatcatgaaatgcagacgaagcacaataatgacttgggt	778
OY	570	gacaattacatcatcctctggtggaagtttgggaaaaagaattacaagaacagctgggaagat	629
Db	779	tactgtgattcttctcgaaaggtcagctgcgatggtccacagacagagaagactgttggggacct	838
OY	630	tgatctagaggtgggtcagtgcacaatgacat	661
Db	839	ggaccttaggtggagcctccacccaataatcagt	870

```

: RESULT 5
: US-09-240-639-5
: Sequence 5, Application US/09240639
: Patent No. 6350447
: GENERAL INFORMATION:
: APPLICANT: Chadwick, Brian Paul
: TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
: TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
: FILE REFERENCE: 9598-066
: CURRENT APPLICATION NUMBER: US/09/240,639
: CURRENT FILING DATE: 1998-01-29
: NUMBER OF SEQ. ID NOS: 29
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 1998
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 45
; LENGTH: 1498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-45

```

```

Query Match      4.0%; Score 60; DB 4; Length 1498;
Best Local Similarity 48.1%; Pred. No. 9, 8e-09;
Matches 233; Conservative 0; Mismatches 245; Indels 6; Gaps 2;

```

```

OY 178 taagcgtatataatgatctgtgtagcactggaagcagagtcacatctctacaatttgat 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 304 taaggagatcatgtttgtagcaggaacgacgacgacgagtaacgcttccagttcacc 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 238 cagaacttagatcctccggttgaaacgaacttgattatattatcgttaaacc 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 364 cggccccccagagaactccacgtaacc--cacgaaccttcaagcagtgaaagcca 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 298 ggtttgattcatagcgtcttaactcctgaagaagctgcagaatccttgattccattcta 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 421 ggtcttctgctatgtgatgtgttgaaagcgtcgaaggaatccggaactactg 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 358 aaagaagcagaagaatgtgttctctgtgagccagcaaccacacccgttaagcttggg 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 481 gatgtgtctaaacagacalcctccgttcgacttctgaaaggcccccctcgtgtccaag 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 418 gcaactgcaggtttaagccttttgaggaggaatgctgctgtaaaatatattgcaagcggtc 477
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 541 gccacagcgtggtcttaagcctgtaactctggaagaagccagagaagttactgcagaaggtg 600
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 478 agggatagctcagcaacagaagtgcccttaagtccaatcagatcagatattctt 537
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 601 aaagaagattttaagcatcgcttcccttgtaggggat--gactgtgttccatcatg 657
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 538 gatggagaccagaagaagttcttattcttgggtgacaataactatctctggggaagttg 537
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 658 aagggagacagatgaaagcgttctcggtggtatccatcactccttgacagagcaagcttg 717
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 598 ggaanaagatttacaagaagcgtggagtagttgattgaagtgaggtggttcagcaaatg 657
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 718 aaaccccgagagagcagcgtggcagatgctgacttggtggagagatccactcagatc 777
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 658 acat 661
    |||||
DB 778 gcct 781
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RESULT 8
US-09-608-285A-53
; Sequence 53, Application US/09608285A
; Patent No. 6335013

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; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 53
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-53

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Query Match      4.0%; Score 60; DB 4; Length 1588;
Best Local Similarity 48.1%; Pred. No. 1e-08;
Matches 233; Conservative 0; Mismatches 245; Indels 6; Gaps 2;

```

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OY 178 taagcgtatataatgatctgtgtagcactggaagcagagtcacatctctacaatttgat 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 451 taaggagatcatgtttgtagcaggaacgacgacgacgagtaacgcttccagttcacc 510
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 238 cagaacttagatcctccggttgaaacgaacttgattatattatcgttaaacc 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 511 cggccccccagagaactccacgtaacc--cacgaaccttcaagcagtgaaagcca 567
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 298 ggtttgattcatagcgtcttaactcctgaagaagctgcagaatccttgattccattcta 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 568 ggtcttctgctatgtgatgtgttgaaagcgtcgaaggaatccggaactactg 627
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 358 aaagaagcagaagaatgtgttctctgtgagccagcaaccacacacccgttaagcttggg 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 628 gatgtgtctaaacagacalcctccgttcgacttctgaaaggcccccctcgtgtccaag 667
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 418 gcaactgcaggtttaagccttttgaggaggaatgctgctgtaaaatatattgcaagcggtc 477
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 688 gccacagcgtggtcttaagcctgtaactctggaagaagccagagaagttactgcagaaggtg 747
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 478 agggatagctcagcaacagaagtgcccttaagtccaatcagatcagatattctt 537
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 748 aaagaagattttaagcatcgcttcccttgtaggggat--gactgtgttccatcatg 804
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 538 gatggagaccagaagaagttcttattcttgggtgacaataactatctctggggaagttg 597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 805 aacggagacagatgaaagcgttctcggtggtatccatcactccttgacagagcaagcttg 864
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 598 ggaanaagatttacaagaagcgtggagtagttgattgaagtgaggtggttcagcaaatg 657
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 865 aaaccccgagagagcagcgtggcagatgctgacttggtggagagatccactcagatc 924
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

QY	658	acat	661
Db	925	gcct	928

RESULT 9
 US-09-608-285A-48
 : Sequence 48, Application US/09608285A
 : Patent No. 6335013
 : GENERAL INFORMATION:
 : APPLICANT: Ford, John
 : APPLICANT: Mulero, Julio
 : APPLICANT: Yeung, George
 : TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
 : TITLE OF INVENTION: POLYPEPTIDES
 : FILE REFERENCE: 28110/36570
 : CURRENT APPLICATION NUMBER: US/09/608, 285A
 : CURRENT FILING DATE: 2000-06-30
 : PRIOR APPLICATION NUMBER: 09/553, 231
 : PRIOR FILING DATE: 2000-05-26
 : PRIOR APPLICATION NUMBER: 09/557, 800
 : PRIOR FILING DATE: 2000-04-25
 : PRIOR APPLICATION NUMBER: 09/481, 238
 : PRIOR FILING DATE: 2000-01-11
 : PRIOR APPLICATION NUMBER: 09/270, 265
 : PRIOR FILING DATE: 1999-08-09
 : PRIOR APPLICATION NUMBER: PCT/US99/16180
 : PRIOR FILING DATE: 1999-07-16
 : PRIOR APPLICATION NUMBER: 09/350, 836
 : PRIOR FILING DATE: 1999-07-09
 : PRIOR APPLICATION NUMBER: 09/273, 447
 : PRIOR FILING DATE: 1999-03-19
 : PRIOR APPLICATION NUMBER: 09/244, 444
 : PRIOR FILING DATE: 1999-02-04
 : PRIOR APPLICATION NUMBER: 09/122, 449
 : PRIOR FILING DATE: 1998-07-24
 : PRIOR APPLICATION NUMBER: 09/118, 205
 : PRIOR FILING DATE: 1998-07-16
 : NUMBER OF SEQ ID NOS: 60
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 48
 : LENGTH: 2693
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-608-285A-48

Db	679	aagagagatattaaagcatgcgttccttcctcttgtagggat---	gactgtgtttccatcatg	735
QY	538	gatgtgaacccaagaagcttctatcctttgggtgacaattactctcttggggaattg	597	
Db	736	aacggacaacagatgaagcgcttctggcgctggtacacacatcaactctccgcgaagcgacttg	795	
QY	538	ggaagaagaattacaagaacactgtggagtaattatctgaaggttggttcagtccaatg	657	
Db	796	aaactccagagagagagacgctgtggcattgtgacttggcggagagatccatccatgac	855	
QY	658	acat	661	
Db	856	gcct	859	

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10 RESULT
11 US-09-608-285A-26
12 ; Sequence 26, Application US/09608285A
13 ; Patent No. 6335013
14 ; GENERAL INFORMATION:
15 ; APPLICANT: Ford, John
16 ; APPLICANT: Mulero, Julio
17 ; APPLICANT: Yeung, George
18 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
19 ; TITLE OF INVENTION: POLYPEPTIDES
20 ; FILE REFERENCE: 28110/36570
21 ; CURRENT APPLICATION NUMBER: US/09/608,285A
22 ; CURRENT FILING DATE: 2000-06-30
23 ; PRIOR APPLICATION NUMBER: 09/583,231
24 ; PRIOR FILING DATE: 2000-05-26
25 ; PRIOR APPLICATION NUMBER: 09/557,800
26 ; PRIOR FILING DATE: 2000-04-25
27 ; PRIOR APPLICATION NUMBER: 09/481,238
28 ; PRIOR FILING DATE: 2000-01-11
29 ; PRIOR APPLICATION NUMBER: 09/370,265
30 ; PRIOR FILING DATE: 1999-08-09
31 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
32 ; PRIOR FILING DATE: 1999-07-16
33 ; PRIOR APPLICATION NUMBER: 09/350,836
34 ; PRIOR FILING DATE: 1999-07-09
35 ; PRIOR APPLICATION NUMBER: 09/273,447
36 ; PRIOR FILING DATE: 1999-03-19
37 ; PRIOR APPLICATION NUMBER: 09/244,444
38 ; PRIOR FILING DATE: 1999-02-04
39 ; PRIOR APPLICATION NUMBER: 09/122,449
40 ; PRIOR FILING DATE: 1998-07-24
41 ; PRIOR APPLICATION NUMBER: 09/118,205
42 ; PRIOR FILING DATE: 1998-07-16
43 ; NUMBER OF SEQ ID NOS: 60
44 ; SOFTWARE: PatentIn Ver. 2.0
45 ; SEQ ID NO 26
46 ; LENGTH: 2762
47 ; TYPE: DNA
48 ; ORGANISM: Homo sapiens
49 ; FEATURE:
50 ; NAME/KEY: CDS
51 ; LOCATION: (148)..(1599)
52 ; US-09-608-285A-26

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QY 298 ggttcgattcatcagctgttaactcctgaagaagctgcagatcctctgattccacttca 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 568 ggccttctgctcctatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 627
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 358 aagaagcagaaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 628 gattgtgttaaacagacgacattccgttcgactctgtgaagcgccaccctctgtccccaag 687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 gcaactgcaggtttaaagcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 688 gccacagctgtgtctacgcctgttacctgtgaagaagcccaagaagttaactgcagaagtg 747
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 478 agggatattgtcagcaacaagaagtgcccttaagttaacatcagatgaactatcttct 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 748 aagaagattttaaagatcgtccttcccttccctgtgtgtgtgtgtgtgtgtgtgtgtgt 804
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 538 gatggaaccacaagaagttcttcttcttcttcttcttcttcttcttcttcttcttct 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 805 aacggaacagatgaagcgcttctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 864
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QY 598 ggaaaaaagatttaacaagaagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 865 aaaaactccagagagagcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 924
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 658 acat 661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 925 gcct 928
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```

```

RESULT 11
US-09-608-285A-52
; Sequence 52, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608, 285A
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583, 231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557, 800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481, 238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370, 265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350, 836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273, 447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244, 444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122, 449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118, 205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 52
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-52

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Query Match 4.0%; Score 60; DB 4; Length 2762;
Best Local Similarity 48.1%; Pred. No. 1.4e-08;

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Matches 233; Conservative 0; Mismatches 245; Indels 6; Gaps 2;
QY 178 tacgcgttatatttgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 237
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Db 451 tacggatcatatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 cgaactatgatctctcctcgttgaagaagcactgtgaatttatgtattcgtgttaacc 297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 511 cggcccccaagagaactctccacgttaacc-----cagaactctcaagcagtgaagcca 567
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 298 ggttcgattcatcagctgttaactcctgaagaagctgtcagaatcttctgtaccacttca 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 568 ggccttctgctcctatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 627
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 358 aagaagcagaaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 628 gattgtgttaaacagacattccgttcgactctgtgaagcgccaccctctgtccccaag 687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 gcaactgcaggtttaaagcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 688 gccacagctgtgtctacgcctgttacctgtgaagaagcccaagaagttaactgcagaagtg 747
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 478 agggatattgtcagcaacaagaagtgcccttaagttaactcagatgcagatctatcttct 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 748 aagaagattttaaagatcgtccttcccttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 804
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QY 538 gatggaaccacaagaagttcttcttcttcttcttcttcttcttcttcttcttcttct 597
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Db 805 aacggaacagatgaagcgcttctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 864
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QY 598 ggaaaaaagatttaacaagaagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 657
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Db 865 aaaaactccagagagagcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 924
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QY 658 acat 661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 925 gcct 928
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```

RESULT 12
US-09-240-639-1
; Sequence 1, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Fritschau, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240, 639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
US-09-240-639-1

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Query Match 4.0%; Score 60; DB 4; Length 2762;
Best Local Similarity 48.1%; Pred. No. 1.4e-08;
Matches 233; Conservative 0; Mismatches 245; Indels 6; Gaps 2;

```

QY 178 tacgcgttatatttgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 451 tacggatcatatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 cgaactatgatctctcctcgttgaagaagcactgtgaatttatgtattcgtgttaacc 297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 511 cggccccagagaactccacgyltaacc--cacgaaccttcaagaagcagtgaaagcca 567
QY 298 ggttgatcatacgtctgaatccctgaagaagctggagaaatctctgattccacttcta 357
Db 568 ggtcttctgctatgctgcatgcatgtttgaaagagcgtctcgggaatccgggaactatg 627
QY 338 aaagaagcagaanaatgtgttctctctgtgagcagcaaccaacacacccgttaagcttgg 417
Db 628 gatgtgttaacagagacatccgtctgactctctgaaagcgcacccctctgtctcaag 687
QY 418 gcaactgcaagtttaagccttttggaagggaaatgctgctgtaataataatattcaagcggtc 477
Db 668 gccacagctggtcttaagcctctgttaactgtgaaagagcccaaggttaactgcaagaagtg 747
QY 478 agggatgctcagcaacaagaagtgcccttaatgttcaatcagatgcaatctatcttct 537
Db 748 aaagaagatttaagaagccttctctctctgttagggat--gactgtgtttccatcatg 804
QY 538 gatggaacccaagaaggtcttctatctcttggtgacaaatlaactctcttggggaaagtg 597
Db 805 aacggaacagatgaagcggttctcggtggaatccacatcaactctctgacagcgagcttg 864
QY 598 ggaagaagattcaagaagcagtggaagtgatgactagtagaggtggtgagtgcaaatg 657
Db 865 aaactccagagagggagcagcggtggcatgctggaacttggtgaggaatccactcagatc 924
QY 658 acat 661
Db 925 gcct 928

RESULT 13
US-09-608-285A-50
; Sequence 50, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 50
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-50

Query Match 4.0%; Score 60; DB 4; Length 2805;
Best Local Similarity 48.1%; Pred. No. 1,4e-08;
Matches 233; Conservative 0; Mismatches 245; Indels 6; Gaps 2;
QY 178 taagcttattatttgatctgtgtaagcactggaagcagatgctataatgttat 237
Db 451 taaggatcatgtttgtgacgaagcactggaacccagatatacgtctccagttcaac 510
QY 238 cagacttaatctccctccggttgaanaagaaacttgagttatgtatgttgtaaac 237
Db 511 cggccccagagaactcccaagyltaacc--cacgaaccttcaagaagcagtgaaagcca 567
QY 298 ggttgatcatacgtctgaatccctgaagaagctggagaaatctctgattccacttcta 357
Db 568 ggtcttctgctatgctgcatgcatgtttgaaagagcgtctcgggaatccgggaactatg 627
QY 358 aaagaagcagaanaatgtgttctctctgtgagcagcaaccaacacacccgttaagcttgg 417
Db 628 gatgtgttaacagagacatccgtctgactctctgaaagcgcacccctctgtctcaag 687
QY 418 gcaactgcaagtttaagccttttggaagggaaatgctgctgtaataataatattcaagcggtc 477
Db 668 gccacagctggtcttaagcctctgttaactgtgaaagagcccaaggttaactgcaagaagtg 747
QY 478 agggatgctcagcaacaagaagtgcccttaatgttcaatcagatgcaatctatcttct 537
Db 748 aaagaagatttaagaagccttctctctctgttagggat--gactgtgtttccatcatg 804
QY 538 gatggaacccaagaaggtcttctatctcttggtgacaaatlaactctcttggggaaagtg 597
Db 805 aacggaacagatgaagcggttctcggtggaatccacatcaactctctgacagcgagcttg 864
QY 598 ggaagaagattcaagaagcagtggaagtgatgactagtagaggtggtgagtgcaaatg 657
Db 865 aaactccagagagggagcagcggtggcatgctggaacttggtgaggaatccactcagatc 924
QY 658 acat 661
Db 925 gcct 928

RESULT 14
US-09-608-285A-54
; Sequence 54, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205

RESULT 15
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

Query Match	3.3%	Score 49.8	DB 1	Length 7218
Best Local Similarity	5.8%	Pred. No. 4e-05		
Matches	24	Conservative	173	Indels 0
				Gaps 0

Oy	444	ggggaatgcgcgtcaaaaatatcttgcgaagcgccaggatcgtctcagaacaaagtcgc	503
Dd	1434	RRR	13757
Oy	504	cctaattgtccaatcacagtgcagtatcatcttctgtgatgaaaccaagaagttcatact	563
Dd	1374	RRR	13158
Oy	564	ttaggtgacaattaacatactctcttgaggaaagttggaaaaagattacaagaacgtggc	623
Dd	1314	RRR	1255
Oy	624	agtagttgacttaagagctgggcacgtgcacaatgcacatatgcactcctaagaacacagc	683
Dd	1254	RRR	1195
Oy	684	taaaatgctccaaaagtacctgaagagaggaaccatacataaagaagcttgttaccca	743
Dd	1194	RRR	1135
Oy	744	gggaagaataatgaccttaatgttcacagttacttgctatggaagaagaacattccg	803
Dd	1134	RRR	10757
Oy	804	tgcgagatttcaagtcgtcgctggctgtctgttaactcttcatttcagcgc	856
Dd	1074	RRRRRRRAATGGCAAGCTCCCTCGACCTGACGCCAAGCTCGGAATTAAATTCTG	1022

Search completed: June 28, 2002, 02:12:39
Job time: 2654 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 01:27:20 ; Search time 1914.35 Seconds
(without alignments)
10498.063 Million cell updates/sec

Title: US-09-657-631-8

Perfect score: 1489

Sequence: 1 aagtcctctctctctctgtag.....cgatcttctctctgctt 1489

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	502.8	33.8	745	10	BG644489
2	489.8	32.9	760	10	BG584413
3	474.8	31.9	652	10	B1270380
4	465	31.2	658	10	B1263104
5	452.8	30.4	625	10	B1272922
6	451.6	30.3	651	10	B1267324
7	446.8	30.0	650	10	BG457694
8	446.2	29.0	659	10	BF639165
9	434.8	29.2	616	10	B1272802
10	433.4	29.1	664	10	B1265005
11	423	28.4	454	9	AU089497
12	419.4	28.2	659	9	BG457472
13	418	28.1	418	9	AV418181
14	413.8	27.8	663	10	B1267321
15	413.4	27.8	680	10	BF641307
16	412.2	27.7	648	10	B1265356
17	410.8	27.6	583	10	BE322878

18	410.6	27.6	660	10	BE325702
19	410.2	27.5	642	10	BG449843
20	409.6	27.5	656	10	B1265733
21	405	27.2	666	10	BG455221
22	403.6	27.1	576	10	B1272477
23	401	26.9	659	10	BF641795
24	400.2	26.9	665	10	B1266953
25	397.8	26.7	651	10	BG449019
26	397.6	26.7	556	10	BF003844
27	397	26.7	633	10	B1265090
28	396.6	26.6	603	9	BE059022
29	395.6	26.6	658	10	BF641625
30	393.8	26.4	685	10	B1271332
31	391	26.3	619	10	B1266386
32	390.6	26.3	603	10	B1266110
33	389.4	26.2	631	10	B1265759
34	386.2	25.9	655	10	B1263495
35	378.8	25.4	597	10	BG449660
36	378.6	25.4	622	10	BF639043
37	376.8	25.3	528	10	BF068331
38	375.2	25.2	648	10	B1266743
39	374.8	25.2	611	10	B1267700
40	374.2	25.1	657	9	AW584530
41	374	25.1	620	10	B1267682
42	373.6	25.1	604	9	AJ388942
43	373	25.1	624	10	BF642432
44	368.4	24.7	586	10	B1265201
45	368	24.7	643	10	BE322347

ALIGNMENTS

RESULT 1	BG644489	745 bp	mRNA	linear	EST 24-APR-2001
LOCUS	BG644489				
DEFINITION	EST506108 KV3 Medicago truncatula cDNA clone PKV3-37M24 5' end,				
ACCESSION	EST506108				
VERSION	BG644489.1				
KEYWORDS	GI:13779601				
SOURCE	EST.				
ORGANISM	Medicago truncatula				
REFERENCE	1 (bases 1 to 745)				
AUTHORS	Vandenbosch, K., Endre, G., Hur, J., Beremand, P., Town, C.D., Bowman, C.L., Craven, M.B., Cho, J., and Fraser, C.M.				
TITLE	ESTs from roots of Medicago truncatula 72 h after Rhizobium inoculation, 2001				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Vandenbosch K Department of Biology Texas A&M University College Station, TX 77843-3258, USA Tel: 409 845 7707 Fax: 409 845 2891 Email: kate@mail.bio.tamu.edu M3928966 rTGR sequence name: MTEBP84TR More information is available at: www.medicago.org Seq primer: SKmod (CTA gaa cta gta gaa CC).				
FEATURES	location/Qualifiers				
source	1..745				
	/organism="Medicago truncatula"				
	/cultivar="genotype A17"				
	/db_xref="taxon:3880"				
	/clone="PKV3-37M24"				
	/clone_1lb="KV3"				
	/tissue_type="Seedling roots"				
	/dev_stage="3 days post-inoculation with Sinorhizobium meliloti"				

/lab_host="E. coli strain XL0R"
 /note="Vector: Bluescript SK-; Site.1: EcoRI; Site.2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0R cells."

BASE COUNT 239 a 132 c 157 g 217 t
 ORIGIN

Query Match 33.8%; Score 502.8; DB 10; Length 745;
 Best Local Similarity 81.8%; Pred. No. 4.1e-120;
 Matches 605; Conservative 0; Mismatches 132; Indels 3; Gaps 2;

QY 85 atgcctctatctctctcccaatctcggaacaacattccatgacgtgaagata 144
 DB 1 ATGCCCTTCAATTTCTTACTCC-ATATCTGGAAACAACATATTACTCA-CTAACCGTA 57
 QY 145 ttactcccaaaaatcaaggaaccaggttacatcatcagctgttatattgtcgtgaag 204
 DB 58 AGATTTCCTCCAAACAAACAACCAATTTCCCTTATGCTGTGTGTTGATGCTGTAGC 117
 QY 205 actggaagcagagtcacatgctcacaatttgatcagaactagatctctcccttgaa 264
 DB 118 ACTGGAAGCCGTCACATGTTTACCATTTTGATCAAACTTAATCTTCTCATGTTGGT 177
 QY 265 aagcaacttgatttatgatctggttaaacccggtttgattcatacgtctgaacct 324
 DB 178 AAAATATTTGGTTTAAATTAACAAACGCCCGTTGATGATACGCGGATTAATCCA 237
 QY 325 gaagaagctgagagatctctccactctcaaaagaagaagaatgtgtccctgtg 384
 DB 238 GAATAAGCTGAAATCTTTTATTCACATTTTAGACAGCAAGAAAGTATGTTCCGAG 297
 QY 385 agccagcaaccacaacacccgttaagcttgaggcaactgcaggtttaagctttgag 444
 DB 298 GATAGCGCTCCAGACACCCATTGACTTGGGCAACAGCAGGTTTAAAGCTTTGAA 357
 QY 445 ggaagatctgtgaaataatattgcaagcggtcagagatagtcagcaacaagaagtc 504
 DB 358 GGGATGCTCTGAAAATAATCTCAATCGGTAAAGGACTTTGTTCAGCAATGAAATGCC 417
 QY 505 cttaatttcaatcagatgcagtactatctctgatgatgaaccagaagcttctatct 564
 DB 418 TTCAATGTTCAACTGATGACAGTTTATTTATGATGGAACCAAGAAAGTTCATCTC 477
 QY 565 tgggtgacaataactatctctcttgagggaagttggaagaattacaagaacagtgga 624
 DB 478 TGGGTGACAGTTAACTATGCAATTTGGGAAATTTGCAAAAAAATTCACAAAAACGTGGGA 537
 QY 625 gtatgtatcaggaggttggtcagtgcaaatgacatatgagctctaaggaacaacagct 684
 DB 538 GTATATGATCTTGGAGGTGATCAGTTCAATGTCATATGACAGTGCATAATATACGCT 597
 QY 685 aaaaatgctccaaaagtaactcgaaggaagagatcatatcaataaagaagctgtactcag 744
 DB 598 AAAATGCTCCAAAAGTTGCTGATGAGGAAGATCATTATTAAGAGCTTGTACTCAG 657
 QY 745 ggaagaataatgaccttatgtcacagtaacttgctgctatgagaagaagaacttcgt 804
 DB 658 GGAATAAATAATGATCTCTATGTCATATGTTACTTACACTTGGTAGAAGCATCTCGA 717
 QY 805 gcagagatttcaaggtcgc 824
 DB 718 GCAGAGATTTGAAAGTCA 737

RESULT 2
 BG584413 760 bp mRNA linear EST 11-APR-2001
 LOCUS
 DEFINITION EST186173 MHAM Medicago truncatula/Glomus versiforme mixed EST

ACCESSION BG584413
 VERSION BG584413.1 GI:13599477
 KEYWORDS EST.
 SOURCE Medicago truncatula/Glomus versiforme mixed EST library.
 ORGANISM Medicago truncatula/Glomus versiforme mixed EST library.
 REFERENCE Eukaryota: mixed EST libraries.
 1 (bases 1 to 760)
 AUTHORS Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
 TITLE ESTs from roots of Medicago truncatula after colonization with Glomus versiforme, 2001
 JOURNAL Unpublished (2001)
 COMMENT Contact: Harrison M.J.
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73401
 Tel: 580-223-5810
 Fax: 580-221-7380
 Email: mjharrison@noble.org
 Noble EST name: N37983e TIGR sequence name: MTDB016TK More information is available at: <http://www.medicago.org>
 Seq primer: Skm0d (CTA gaa cta gta gat cc).
 Location/Qualifiers
 1. 760
 /organism="Medicago truncatula/Glomus versiforme mixed EST library"
 /cultivar="Medicago truncatula genotype Al1"
 /db_xref="taxon:119092"
 /clone_lib="PMHAM-1507"
 /clone_1ib="MHAM"
 /tissue_type="roots colonized with Glomus versiforme"
 /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
 /lab_host="E. coli strain XL0R"
 /note="Vector: Bluescript SK-; Site.1: EcoRI; Site.2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0R cells."

BASE COUNT 241 a 143 c 153 g 223 t
 ORIGIN

Query Match 32.9%; Score 489.8; DB 10; Length 760;
 Best Local Similarity 80.6%; Pred. No. 1e-116;
 Matches 599; Conservative 0; Mismatches 137; Indels 7; Gaps 2;

QY 67 acccttggttcaatgtaagctcgtcatctctccccaatctccggaacaacatt 126
 DB 24 ACTGTTCTACTCTTTAAATGCTTCGCAATCTCCACAAATATTTAGGAAACCACTA 83
 QY 127 ctcatgactgtaagatattactcccaaaaatcaggaacaggttacatcatcagctgt 186
 DB 84 CTCACTAATCGAAGATTTT-----CCAAAACAACAAACAATTTCTCTTAAGCTGTC 137
 QY 187 atattgatgctgtaagcactggaagcagagtcacatgtctacaatttgatcagaacta 246
 DB 138 GTGTTTATGCTGTACACATCGTAGCCGATTCATCATGTTTACATTTTGATCAACACTTA 197
 QY 247 gatctccctccggttgaagaacacttgagttatgatttcoggttaaacccggttga 306
 DB 198 GATCTTCTTCAATATTTGCCAAAGATGTTGAGTTTAAATGAATMAACCTGGTTTAGT 257
 QY 307 tcatagctgcttaatcctcgaagaagctcagaaatctctgattccactctcaagaagca 366
 DB 258 TCATATGCAAAATGATTCGGAACAAAGCTGCAAAATCTTTGATTCCTTACAAACAAGCA 317

ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
1 (bases 1 to 658)
Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
JOURNAL COMMENT
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 658 Std Error: 0.00
Plate: 038 row: F column: 11
Seq primer: TCACACGAGAAACAGCTATGAC.
Location/Qualifiers
1..658
/organism="Medicago truncatula"
/db_xref="taxon:3880"
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/issue_type="leaf"
/dev_stage="trifoliolate"
/note="Vector: Lambda Zap: At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20um potassium phosphate. RNA was prepared from above ground tissues."
BASE COUNT 214 a 118 c 150 g 174 t 2 others
ORIGIN

Query Match 31.2%; Score 465; DB 10; Length 658;
Best Local Similarity 83.1%; Pred. No. 2.8e-110;
Matches 528; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 295 cccgggttggtatcatcgctgcctcaatccggaagaagctgcgaatctctgattccactt 354
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DB 16 CCCGTTTGATGATCATGCGGGATATCCAGAAACATCTTGATTCACACTT 75
QY 355 ctaaaagaacagaaatggttcctcctgtgacagcaacccaacacccgttaagctt 414
|||||
DB 76 TTAGAGCAGAGAGAAATGTAGTCTCGAGATCAGCGCTCCAAAGACACCATTTAGACTT 135
QY 415 ggggcaactgcaggtttaaggtcttggaggagaaatgctgctgaataatattatgcaagc 474
|||||
DB 136 GGGGCAACACAGAGTTTAAAGCTTTGAATGGGATGCTCTGAAAAAATATCTGCATCG 195
QY 475 gtaaggatattgcctcagaacagaagtccttaattcaatcagatgcagatctattc 534
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DB 196 GTAAAGGATTTGTTACCAATAGAAAGTCACTTCAATTTCAACCTTGATGCAAGTTTCTATT 255
QY 535 ctgatgaaacccaagaagttcttattcttgggtgagcaattactctctctgggggaag 594
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DB 256 ATGATGAGAACCAAGAGTTCTTATCTGTGGTGACATTTAATCTTGATTTGGGAAA 315
QY 595 ttgggaaaagattcaaaagacagtgaggatagttatctagagggtgggtcagtgcaa 654
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DB 316 TTGGGAAAAAATTTCACAAAACAGTGGAGTATGATCTTGAGAGTGATCAGTTTCA 375
QY 655 atgacatattgcaatctcagaagaacagctcaaaatgctccaaagttacctgaaggagag 714
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DB 376 ATGGCAATATGCACTGCTCAAGTATACAGTAAATGCTCCAAAAGTGTCTGATGGAGAA 435
QY 715 gatccatataaagaagctgttactccagggaagaataatgactttatgttcagct 774
|||||

DB 436 GATCCATACATTAGAAAGCTTGACTCAAGSGAAAAAATATGATCTGTATGTCATAGT 495
QY 775 tacttgctatggaagaagactttcgtcagaagatttcaaggtcgtgtgtctt 834
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DB 496 TACTTACACTTTGGTATGAGAGACATCTCGACCAAGATTTTGAAGTTCACACATTAATCT 555
QY 835 gctatccctgcatatttagcgtgcttgatgagcatatattccggagcagat 894
|||||
DB 556 CCCAACCTTGATTTTATGCTGGATTTGATGGACATACATATGCTGGANNAATTTT 615
QY 895 aaggtctggcccaagcttaagatctaactgaa 929
DB 616 AAGGCCAATGCCCTGCTTCTGAGACCAATTTTAA 650

RESULT 5
BI272922
LOCUS
DEFINITION
NF091F05FLJ1046 Developing flower Medicago truncatula cDNA clone
ACCESSION
BI272922
VERSION
BI272922.1 GI:14882668
KEYWORDS
EST.
SOURCE
barrel medic.
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
1 (bases 1 to 625)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula flower library
Unpublished (2001)
JOURNAL COMMENT
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 625 Std Error: 0.00
Plate: 091 row: F column: 05
Seq primer: TCACACGAGAAACAGCTATGAC.
Location/Qualifiers
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/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone_id="NF091F05FL"
/issue_type="Developing flower"
/dev_stage="Developing flowers"
/note="Vector: Lambda Zap: cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the uni-zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant uni-zap XR vector using ExAssist helper phage and the E. coli strain XL1-blue MRP' (Stratagene). Excised plasmids were plated using SOUR cells."

BASE COUNT 205 a 110 c 140 g 169 t 1 others
ORIGIN

Query Match 30.4%; Score 452.8; DB 10; Length 625;
Best Local Similarity 82.7%; Pred. No. 4.2e-107;
Matches 517; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

```

OY 312 cgcgttaacccctgaagaagctgcagaatcctcgtatccactcttaagaagaacagaa 371
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Db 1 CGGGATTAATCCAGAAAGAGCTGCAAAATCTTGATTCACCTTTTGAGACACAGAAAG 60
OY 372 tctgtctctgtgagccgaacacacacacccgttaagcttggggcaactgcagttt 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TGTAGTCTCGAGGATCGAGCGCTCCAGAACCCCATTAAGCTAGGGGCAACAGCAGTTT 120
OY 432 aagccttctggagggaatgctgtcgaataatattgtcaagcgttcaggatattgctcg 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 AAGGCTTTGGAATGGGAGATGCTTCTGAAAAAATACGCAATCGGTAAGGATTTGTTACG 180
OY 492 caacagaagtcaccttaatgctcaacacagatcagatcattctgtatggaacccaaga 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 CATATAAGAGACTTCAATGTTCAACCTGATGAGTTCATATTATGATGGAACCCAGAG 240
OY 552 aggttctatcttctgggtgacaataactatctctcttgggggaagcttgggaanaagattac 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 AGGTCTTATCTCTGGGTGACAGTTAATGATGATTGGGGAATTTGGAAAAAATTTAC 300
OY 612 aaagaagaatgggagatgctgataagagtggtgagtggaatgacataatgagcttc 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 AAAAAGGAGGAGTATGATGATCTTGAGAGTGATCATGTTCAATGCGCATATGACAGTGC 360
OY 672 aaggaacacagactaaatgctcacaagaatgacagagagagagatccatataagaag 731
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 AAAGTATACAGCTAAATAATGCTCCAAAAGTGTGATGAGAGATCCATACATTAAAGAA 420
OY 732 gcttgactccaggaaagaataatgaccttctatgctcagacttacttgcgtatggaag 791
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 GCTTGACCAAGGAAAAAATATGATGCTCTATGTTTCAATGTTACTTACACTTTGGTAG 480
OY 792 agaagaattctgtgcagaatcttcaagctcgtgtgtgttctgcgtcaactcgtcattt 851
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 AGAAGATCTCGAGCAGAAATTTTGAAGTCACACATTAATTCGCCAACCCCTTGACATTTT 540
OY 852 agctgcttctgagtgagcatatcatatccgagcagagatgaagcttcgcccagc 911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 AACTGATTTTGAATGGGACATACATATGCTGAGAGAAATTTAAAGCCCAATGCCCTGC 600
OY 912 ttcagacttaacttgaatcaatgc 936
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 TTCTGGAGCCAAATTTTAAAAAATGC 625

RESULT 6
BI267324 651 bp mRNA linear EST 18-JUL-2001
LOCUS NF105B12IN1F1101 Insect herbivory Medicago truncatula cDNA clone
DEFINITION NF105B12IN 5', mRNA sequence.
ACCESSION BI267324
VERSION BI267324.1 GI:14872249
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 651)
REFERENCE 1 (bases 1 to 651)
AUTHORS Korth,R., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
,H.R., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula insect herbivory library
Unpublished (2000)
CONTACT: Korth R
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
Email: Kkorthcomp.uark.edu

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FEATURES
    source
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            /organism="Medicago truncatula"
            /db_xref="taxon:3880"
            /clone="NF105B12IN"
            /clone_lib="Insect herbivory"
            /tissue_type="local and systemic leaves"
            /dev_stage="mature"
            /note="Vector: Lambda Zap; library was produced from fully
            expanded M. truncatula leaves of plants fed upon by
            Spodoptera exigia (beet armyworm) for 24 hours. Systemic
            (undamaged leaves from injured plants) and wounded leaves
            were harvested and pooled."

BASE COUNT      208 a      114 c      142 g      187 t

ORIGIN
Query Match      30.3%; Score 451.6; DB 10; Length 651;
Best Local Similarity 83.3%; Pred. No. 8,7e-107;
Matches 525; Conservative 0; Mismatches 104; Indels 1; Gaps 1;

OY 156 aaatcagaacacagttacatcatcagctgtatattgtatgctgtgagca-ctggaagca 214
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 22 AAACAAGAACCAATTTCCCTTATGCTGTGTGTTGATGAGCTGAGACCTGGAAGCC 81
OY 215 gaqtcagctctacaatttgcatacagaacttagatctcctccgttgaacagcaactg 274
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 82 GTGTCATGTTTACATTTTGTATCAAAACTTAATCTTCTTCATGTTGTAAGATGTTG 141
OY 275 agttatgatctggttaaacccggtttagatcagctgtcatcgttaactcgaagaagctg 334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 142 AGTTTATATATAGACAAAGCCCGGTTTGATGCTATPACGGGTAATCCAGAAAGCTG 201
OY 335 cagaatctctgattccactctctaaagaagaagaatgtygtctctgtgagccaagc 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 202 CAATAATCTTTGATTTCCACTTTTAGAGCAACCAAGAGTGTACTCTGAGAGATCAGCGCT 261
OY 395 ccaacacaccggttaagcttggggcaactgcaagtttaagcttgggaagggaatgctg 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 262 CCAAGACACCCATTAGACTTGGGGCAACAGCAGGTTTAAGGCTTTGAATGGGAGATGCTT 321
OY 455 ctgaaatatattgcaagcgttcagggatattgctgcgaacaaagtcccttaatgctc 514
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 322 CTGAAAAAATACATGCAATGCGTAAGGATTTGTTACGCAATAGAGTACTTCAATGTTTC 381
OY 515 aatcagatgagatcatctatcttgcagtggaacccaagaagttcttacttgggtgacaa 574
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 382 AACCTGATGAGTTCATATTATTATGATGGAACCAAGAGAGTCTTATCTCTGGGTGACAG 441
OY 575 ttaactatctcttggggaagttgggaanaaagattcaaaagacagtgggaagtattgac 634
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 442 TTAACATGATGATGGGGAATTTGGGAAAAAATTCACAAAAACAGTGGGAGTATGATGC 501
OY 635 taggaagtgtgtagcgaataatgacatgcaatcccaaggaacaaagcctaaatgctc 694
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 502 TTGGAGGTGATGATGTTCAAAATGGCATATGCAATGCTCAAGATVACAGCTAAATAATGCTC 561
OY 695 caaaagctacgtgaagagagagatccatataagaagaagcttgcaccagggaaagaat 754
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 562 CAATAATGCTGTGATGAGAGAGATCCATACATTAAAGAGCTTGATCAAGGAAAAAAT 621
OY 755 atgaccttaatgctcagttactgctc 784
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Db 622 ATGATCTCTATGTTCAATGATTAAGTACTTACACT 651

RESULT 7
BG457694 650 bp mRNA linear EST 19-MAR-2001
LOCUS BG457694
DEFINITION NF106E11P1F11085 Phosphate starved leaf Medicago truncatula cDNA

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ACCESSION      clone NF106E11PL 5', mRNA sequence.
VERSION        BG457694
KEYWORDS       BG457694.1  GI:13381019
SOURCE        EST
ORGANISM       barrel medic.
               Medicago truncatula
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
               Medicago.
REFERENCE      1 (bases 1 to 650)
AUTHORS       Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
               H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE         Expressed Sequence Tags from the Samuel Roberts Noble Foundation
               Medicago truncatula phosphate-starved leaf library
JOURNAL       Unpublished (2000)
COMMENT       Contact: Harrison MJ
               Plant Biology Division
               The Samuel Roberts Noble Foundation
               2510 Sam Noble Parkway, Ardmore, OK 73402, USA
               Tel: 580 221 7325
               Fax: 580 221 7380
               Email: mharrison@noble.org
               Insert Length: 650      Std Error: 0.00
               Plate: 106      row: E      column: 11
               Seq primer: TCACACGAGAAACACGCTATGAC.
               Location/Qualifiers
               1..650
               /organism="Medicago truncatula"
               /db_xref="taxon:3880"
               /clone="NF106E11PL"
               /clone_1lb="Phosphate starved leaf"
               /tissue_type="leaf"
               /dev_stage="trifoliolate"
               /note="Vector: Lambda Zap; At the trifoliolate stage, M.
               truncatula plants were transplanted to phosphate-free sand
               and grown for a further 30 days. During this 30 day
               period, the plants were fertilized twice weekly with 1/2
               Hoaglands solution containing only 20uM potassium
               phosphate. RNA was prepared from above ground tissues."

BASE COUNT    211 a      110 c      153 g      176 t
ORIGIN
Query Match      30.0%; Score 446.8; DB 10; Length 650;
Best Local Similarity 81.5%; Pred. No. 1.6e-105;
Matches 517; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

OY 265 aacgaacttgagtttatgattcggttaaacccggttggaattcatacgtgctaactcct 324
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11 AACGATGTTGAGTTTAAATTAAGCAACACCCGCTTGAAGTGCATACGCGATATATCCA 70
OY 325 gaagaagctgcagaatcctctgattccactctaaagaagcagaagaatgtgttcctgtg 384
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 71 AAGGAGACGAGAGAGTCTCTGATTCCACTTTTAAAGCAGACAGAAAGAGTGTCTCTGTT 130
OY 385 agccaagaccacaacaccccggttaagcttggggaactgcaggctttaaaggcttggag 444
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 131 AATCTGCACACCAACCAACCCGCTTAAGCTTGGGCAACAGCCGCTTAAGCCTTTTGAT 190
OY 445 gggagactcgtcgtgaataatattatgcgaacggtcagagatatgctcacacaagaagtc 504
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 191 GGAATATCTTCGGAATTAATTTGGAAGCGGTGTCGAGTTTGCTCAAAAAGAGAGCAGC 250
OY 505 cttaattcgaatcagaatgcagtaattctatcttgatgaaagcacaagaagttctatcct 564
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 TTTAAGCTACATCAGATGAGTAGAATTAATTGATGTTACACAGAAAGTTCTTATTATTA 310
OY 565 tgggtgacaattactatctctctggggaagttgggaaagaattacaaagaacgtggga 624
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 311 TGAGTGCAATTAATTAATGTTTGGGAAACCTTGGGAAAGATTTTTCAGAGACAGTGCGCA 370
OY 625 gtaagtatctaggaagtggtgcagtgcaaatgacatatgcatgctcctaaggaacacagct 684

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Db 371 GTAGCTGATCTTGGAGGGGGATCAGTTCAAAATGATATATGATCTCAAGGAACAAGCA 430
OY 685 aaaaatgctccaaaagtlaccctgaaggaagagatccatacataaagaagctgtactccag 744
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 431 AAAAAGCTCCACAAAGTACCTCCAGGAGAGATCCATATCAATAAAAAGATTGTACTTAA 490
OY 745 ggaagaagaatctgaccttattgttccaaagttacttcgcgtatggaagaagaacattcgt 804
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 491 GGAAGAAGAAATATACCTCTATGTTCCACAGTATTTGGGTTGGCAAGAAGCATCTCGT 550
OY 805 gcaagatcttcaaggtcgcgtgtgtcttcgtactaatcttcgacttgaagctgttgat 864
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 551 GCTGAATTTTGAAGAAGTACATCAATAGTGTCTTCTTAATCTTGCAATTTAGCTGGCTATCAT 610
OY 865 gggacatacatattccgcgagcagagatlaag 898
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Db 611 GGCACATATACATATTCAGAGAGAGAGTATTAAG 644

RESULT      8
LOCUS       BF639165                      659 bp      mRNA      linear      EST 19-DEC-2000
DEFINITION  NF094A12PL1P1087 Phosphate starved leaf Medicago truncatula cDNA
VERSION     BF639165
KEYWORDS    BF639165.1  GI:11903323
SOURCE      EST.
ORGANISM    barrel medic.
             Medicago truncatula
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
             Medicago.
REFERENCE   1 (bases 1 to 659)
AUTHORS    Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
             H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE      Expressed Sequence Tags from the Samuel Roberts Noble Foundation
             Medicago truncatula phosphate-starved leaf library
JOURNAL    Unpublished (2000)
COMMENT    Contact: Harrison MJ
             Plant Biology Division
             The Samuel Roberts Noble Foundation
             2510 Sam Noble Parkway, Ardmore, OK 73402, USA
             Tel: 580 221 7325
             Fax: 580 221 7380
             Email: mharrison@noble.org
             Insert Length: 659      Std Error: 0.00
             Plate: 094      row: A      column: 12
             Seq primer: TCACACGAGAAACACGCTATGAC.
             Location/Qualifiers
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             /db_xref="taxon:3880"
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             /clone_1lb="Phosphate starved leaf"
             /tissue_type="leaf"
             /dev_stage="trifoliolate"
             /note="Vector: Lambda Zap; At the trifoliolate stage, M.
             truncatula plants were transplanted to phosphate-free sand
             and grown for a further 30 days. During this 30 day
             period, the plants were fertilized twice weekly with 1/2
             Hoaglands solution containing only 20uM potassium
             phosphate. RNA was prepared from above ground tissues."

BASE COUNT    208 a      114 c      151 g      180 t      6 others
ORIGIN
Query Match      30.0%; Score 446.2; DB 10; Length 659;
Best Local Similarity 80.1%; Pred. No. 2.2e-105;
Matches 520; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

OY 265 aacgaacttgagtttatgattcggttaaacccggttggagttcatacgtgctaactcct 324

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Db 11 AACGATGTTGATTTATTAATAGACAACACCCGTTTGATGCAATACGAGATAATCA 70
Qy 325 gaagaagctgcagaatctctgattccactctctaaagaagagaatggtctctg 384
Db 71 AAGGACAGCAGAGCTCTGATTCACCTTTTACAGCAGAGAGAAAGGTTCTCTGTT 130
Qy 385 agccagcaaccacacacccgcttaagcttgaggcaactcaggtttaagccttggag 444
Db 131 AATTGCAACCCCAAAACACCGTTAGCTTGCGCAACAGCCGGTTTAAGGCTTTGAT 190
Qy 445 ggaatgctgcgtgaataatatactgcaagcgtgagagatactccacagaagaagtcgc 504
Db 191 GGAATTTCTTCCGAAATGATATTTGGAAGCGGTGCGAGTTTGCTCAAAAAGAGACAGC 250
Qy 505 cttaattcaatcagatgcagtaactctctctgtagaagcaagcaaggttctatctt 564
Db 251 TTTACGCTACATCAGATGCGAGTGAATTAATGATGTCACAAAGAGGTTCTTATTTA 310
Qy 565 tgggtgcaattactatctctcttgaggagcttgaggaaagatttacaagaagcagttgga 624
Db 311 TGGGTGACATTTAATCTATGTTTGGAAACTTGGAAAGATTTTTCAGAGACAGTGCA 370
Qy 625 tgaattgactgaggaggtgggtcagtgcaaatgacatactcagctcagaagaagcagct 684
Db 371 GTACTGATCTTGGAGGGGATCAGTTCAATGATATGATGACATCAAGAGAACAGCA 430
Qy 685 aaaaatctccaaaagactctgaaagagagagatccatacataaagaagctgtctcag 744
Db 431 AAAAATCTCCACAAAGACCTCAGGAGAGATTCATCAATAAAAGATTGTACTTAA 490
Qy 745 ggaagaataatgaccttaattgttcacagttactgctgataagagaagaagcttcgt 804
Db 491 GGAAGAATATTTACCTCTATGTTCCACAGTATTTGGCGTTTGGCAANNAAGATCTCGT 550
Qy 805 gcagagatttcaagctgcgtggtgtctctgatacccttgatcttaagctgtctgag 864
Db 551 GCTAAATTTTGAAGAGTCACATTAATGTTCTCTATCTTCATTTTANCTGCTATCAT 610
Qy 865 ggagcatatatacttcgcagagcagagataagctctcgcgccagctt 913
Db 611 GGCACTATTCATATTCAGAGAGAGATNTNAGCATTTTCTCTCTCT 659

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RESULT 9
LOCUS B1272902 616 bp mRNA linear EST 18-JUL-2001
DEFINITION NF098609FL1071 Developing flower Medicago truncatula cDNA clone
ACCESSION B1272902
VERSION B1272902.1 GI:14882630
KEYWORDS EST.
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 616)
AUTHORS Flores-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
TITILE Flores, R.R., Imman, J.T., Weller, J.W. and May, G.D.
JOURNAL Medicago truncatula flower library
COMMENT Medicago truncatula flower library
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
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FEATURES
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/clone="NF098609FL"
/issue_type="Developing flower"
/dev_stage="Developmentally pooled. Contains a mixture of
very young, developing, fully-opened flowers and flowers
in early transition into pods."
/notes="Vector: Lambda Zap; cDNA was prepared from polyA+
RNA from very young, developing, fully-opened flowers and
flowers transitioning into pods. The cDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinant Uni-Zap XR vector
using ExAssist helper phage and the E. coli strain
XL1-Blue MRF' (Stratagene). Excised plasmids were plated
using SOLAR cells."
BASE COUNT 194 a 96 c 137 g 187 t 2 others
ORIGIN
Query Match 29.2%; Score 434.8; DB 10; Length 616;
Best Local Similarity 81.5%; Pred. No. 2e-102;
Matches 502; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
Qy 452 ctgctgaaatatatgcaagcgtgacagagatagtcgaagcaagagtccttaagt 511
Db 1 CTTCGAAAAGATATCTGCAATCGGTAGGATTTGTTGACCAACAGAAATCACTTCAATG 60
Qy 512 ttaactagatgcagatctatctctgtagaagcaagagagcttctatcttgggtga 571
Db 61 TTCAACCTGATGCGATTTTATTAATGATGAAACCAAGAGGTTCTTATCTATGCTGA 120
Qy 572 caattaactatctcttgaggaggttgaggaaagattacaagaagcagtgaggatgtg 631
Db 121 CAGTTAACTATGCAATTTGGGACTTTGGGAAAATTTCACAAAACAGTGAGTAATGG 180
Qy 632 atctaagaggttggtcagtgcaaatgacatactcagctcctaagaagacacagctaaatg 691
Db 181 ATCTGGAGGTGATCGCTTCAATGATGCAATGATGCAATGCAATGCAATGCAATGCAATG 240
Qy 692 ctccaaagtaactgaaagagagatccatacataaagaagctgtctcaccaggaaaga 751
Db 241 CTCCAAAAGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Qy 752 aataagccttatagttcacagttactgctgctatggaagaagcattcgtgagaga 811
Db 301 AATATGATCTCTATGTTCAATGTTACTTACACTTGTGTAAGAGCAATCTGGGCTGAGA 360
Qy 812 ttctcaagctgcgtggtgtctctaatccttgcatctttagcttgctttagatggagcat 871
Db 361 TTTTGAAGGTGATCAGCAATATTTCTCTAACCTTTCATTTAGTGAGTTTGAAGGAGCAT 420
Qy 872 atacatactcgaagcagagataaggtctcgccccaagcttcaagatctaatgcatc 931
Db 421 ACAATATGCTGTGGAAGAAATTTAAGGCCCAATGCCCTTCTGAGGCCAGTTTAAAA 480
Qy 932 aatgcagaagaatgccttaagcctttaaagtgaaatgcaactgtgacctatcaagatt 991
Db 481 AATGCAAAAGATATGTTCAATCAGGCTTTAATATTGAATATCCATGCTTATCAAAATT 540
Qy 992 gcaatttggtgagataggaatggtgaggttggaagtggtcacaataatcttctctta 1051
Db 541 GCACTTTTGGGAAATTTGGAATGCTGAGGAAGAAANTGGACANMAAACTTTTCTGCTG 600
Qy 1052 ctcaatcttctatata 1067
Db 601 CTTCATTTTCTTTTAA 616

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REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
1 (bases 1 to 454)	Endo, M., Kokubun, T., Takahata, T., Higashitani, A., Tabata, S. and Watanabe, M.	Analysis of expressed sequence tags of flower buds in <i>Lotus japonicus</i>	DNA Res. 7, 213-216 (2000)		
20363098	Contact: Masao Watanabe	Fac. of Agri.	Iwate University	3-18-8 ueda, Morioka, Iwate 020-8550, Japan	Tel: 81-19-621-6152 Fax: 81-19-621-6177 Email: mabe@iwate-u.ac.jp
This clone was obtained from a 5' end.					
Location/Qualifiers					
1. 454					
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/db_xref="taxon:34305"					
/clone="Ljfb-u31"					
/clone_id="Lotus japonicus flower bud cDNA"					
/tissue_type="mature flower bud"					
/lab_host="SOLR"					
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; variety-Gifu B-129; Plants of <i>Lotus japonicus</i> Gifu B-129 were grown in a greenhouse condition. Sepal was removed from flower bud. The mRNA was isolated from flower bud of 0.7-1.0cm in length just before anther dehiscence."					
130 a	101 c	89 g	133 t	1 others	

Query Match 28.4%: Score 423; DB 9; Length 454;

Best Local Similarity 99.3%: Pred. No. 2.2e-99;

Matches 445; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

OY 24 gtgcattgactgaagcatgcatgcttctaataatgcatcgaacttggctgcatgt 83
 Db 9 GTTGCAATGGACTAAAGCCATGACCTTCTTAATTAATCAATGACCTTGTGTCATGTT 68
 OY 84 aatgctgtatctcttccccaatcgcgaacacacatcctcgaatcgaatcgaat 143
 Db 69 AATGCTGTATCTCTCTCCCAATATCTCGAAACAACATCTCATGATGTAAGAT 128
 OY 144 attaccctcccaaaatcaggaacaggttaacatatacgcctgtatatttgatgctgtag 203
 Db 129 ATTACTCCCCCAAAATCAGGAACCACTTACATCATACGCTGTAATTTGATGCTGTAAG 188
 OY 204 cactggaagcagaagtcacatgctctacaaatttgatcagaacttagatcctccctgtag 263
 Db 189 CACTGGAAGAGAGTCATGTCATGTCATCAATTTTGTATCAGAACTTGAATCTCCTCCGTTGA 248
 OY 264 aaacgaacttgagtttataatgattcgggttaacccgggttgagttcgaatcgaatcgaatcc 323
 Db 249 AAACGAACCTTGAATTTATGATTCGGTTAAACCCGGTTGAGTTCAATGACCTCTAATCC 308
 OY 324 tgaagaagctgcaagatctctgattcgaacttcaagaagaagcaagaatggtgcttctgt 383
 Db 309 TGAAGAA-CTGCGAATCTCTGATTCACCTTCTAAAGAA-CAGAAATGTGTTCTCTGT 366
 OY 384 gagcgaagcaccacacacacccggttaagcttggggaactgcaagtttaagccttggtag 443
 Db 367 GAGCCANCAACCCACACACACCCGTTAAGCTTGGGCAACGACGTTTAAAGCTTTTGA 426
 OY 444 ggggaatgctgctggaataatattgcaa 471
 Db 427 GGGGAATGCTGTGAATAATATTGCA 454
 RESULT 12
 LOCUS BG457472 659 bp mRNA linear EST 19-MAR-2001
 DEFINITION NF106A03PL1F1019 phosphate starved leaf Medicago truncatula cDNA
 ACCESSION BG457472
 VERSION BG457472.1 GI:13380893
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 659)
 REFERENCE Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
 H.R., Imman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula phosphate-starved leaf library
 COMMENT Unpublished (2000)
 CONTACT: Harrison MJ
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7325
 Fax: 580 221 7380
 Email: mharrison@noble.org
 Insert Length: 659 Std Error: 0.00
 Plate: 106 row: A column: 03
 Seq primer: TCACACAGCAAAACAGCTATGAC.
 FEATURES
 source
 1..659
 Location/Qualifiers
 /organism="Medicago truncatula"
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/clone="NF106A03PL"
 /clone.lib="phosphate starved leaf"
 /tissue_type="leaf"
 /dev_stage="trifoliolate"
 /note="Vector: Lambda Zap. At the trifoliolate stage, M.
 truncatula plants were transplanted to phosphate-free sand
 and grown for a further 30 days. During this 30 day
 period, the plants were fertilized twice weekly with 1/2
 Hoaglands solution containing only 20mM potassium
 phosphate. RNA was prepared from above ground tissues."

Query Match 28.2%: Score 419.4; DB 10; Length 659;
 Best Local Similarity 78.8%: Pred. No. 2.1e-98;
 Matches 514; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

OY 557 ctatctctgggtgagcaatatactctcttggggaagtggaagaaagattacaaga 616
 Db 8 CTATCTCTGGGTGACAGTTAACTATGCAATGGGAAATTTGGAAATAATTCACAAAAA 67
 OY 617 cagtggaagtagttgatacagaagtggtgcagtgcaaatgacatatcgaactcaaga 676
 Db 68 CAGTGGAGTAATGATCTTGGAGGTGATCAGATTCAAATGGCATATGCAAGTGTCAAACT 127
 OY 677 acacagctaaatgtctccaaagtaactcgtgaagagagagatccatatacaagaagcttg 736
 Db 128 ATACAGCTAAAAATGCTCCAAAAGTTGCTGATGAGAGAAATCCATATTAAGAACTTG 187
 OY 737 tactccagggaaagaataatgaccttattgctacagttacttgcgtataggagaag 796
 Db 188 TACTCAAGGAAAAAATATGATCTGATGATCATGATTAATCACTTGTGAGAGAG 247
 OY 797 catttgagcagaagattccaaggtgcgtggtgttcgtatcccttgcatctttagctg 856
 Db 248 CATCTTGACACAGATTTTGAAGGTGCACATTAATCTCCAAACCTTCATTTTAACTG 307
 OY 857 gcttgaatgggcataatactatccggagcagagataagttctcgcccaagcttag 916
 Db 308 GATTTGATGGACATACATATATGCTGAGAGAAATTTAAAGCCAAATGCCCTGCTTCTG 367
 OY 917 gatcctaactgatacagacagagaatagctcttaagctcttaagatgacacatt 976
 Db 368 GAGCCAAATTTTAAAAAATGCAAAAAGATAGTTCGATGAGCTCTTAATTAATTAATCAAT 427
 OY 977 gtccctataagaattgacatttgggtggaatagaaatggtggaggtggaagtgtgcaaa 1036
 Db 428 GTCCCTATCAGAAATTCACCTTTTGGTGAATTTGGAGTGTGAGGAGGAGATGACAGCA 487
 OY 1037 aaatctttcttactatcttcttactactctctcgaagatggttgagcttgtga 1096
 Db 488 GAATACCTTTTGTCTGTATCTTTTAACTTACCTGAAGATATGCTTGTGTGACC 547
 OY 1097 ataacc-----caatgccaataatcgtccagttatggaagctgagcgaataag 1150
 Db 548 CAATATCATTATATATCTCAGCACTTCGTCCTGTGATCTTGAGATGCAAGCAATAAAG 607
 OY 1151 ctgttaaaaacaaatcttgagatgacaaatcccaataccagatcctttaga 1202
 Db 608 CTGTACATTAAATCTTGANAGGCAAAATCACTTATCCACTTCCTTGTGGA 659
 RESULT 13
 LOCUS AV418181 418 bp mRNA linear EST 23-MAY-2000
 DEFINITION AV418181 Lotus japonicus young plants (two-week old) Lotus
 japonicus cDNA clone M1153g11_r 5', mRNA sequence.
 ACCESSION AV418181
 VERSION AV418181.1 GI:7747359
 KEYWORDS EST.
 SOURCE Lotus japonicus.
 ORGANISM Lotus japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.

REFERENCE 1 (bases 1 to 418)

AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
JOURNAL DNA Res. 7 (2), 127-130 (2000)
MEDLINE 20277479

COMMENT

Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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Email: ynakamu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers

FEATURES
SOURCE

1. 418
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MM153j11_r"
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/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; isolate=Myakojima MG-20"
BASE COUNT 121 a 81 c 99 g 117 t
ORIGIN

Query Match 28.1%; Score 418; DB 9; Length 418;
Best Local Similarity 100.0%; Pred. No. 4.4e-98;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 attgatgctgtgacactggaagcagatgcacatgctacattgtatcagaactaga 248
DB 1 ATTGATGCTGTGACACTGGAAGCAGATGCATGCTACATTTTGATCGAAGCTTGA 60
QY 249 tctctcccggtgaaacgaactgattatgattcggttaaacccggttgatc 308
DB 61 TCTCTCCCGGTTGAAACGAACTTGATTGATTCGGTTAAACCCGCTTGAAGTTC 120
QY 309 atagcgtcattcctgaagaagctgcaagatcctcattccactcttaagaagcaga 368
DB 121 ATAGCGTCTATCTCTGAGAGAGCTGCAAGATCTCTGATTCACCTTCTAAAGAGAGA 180
QY 369 aaatggttcctgtagccagcaaccacacaccccggttaagcttggggcaactgca 428
DB 181 AAATGTTGCTCTGAGACCGCAACCAACACACCGCTTAAAGCTTGGGCACTGAGG 240
QY 429 tttaagccttttgaggagggaatgctgctgaaatataatttcgaagcggatcagga 488
DB 241 TTTAAGCCTTTTGGAGGGGAATGCTGCTGAAAATATATTTGCAAGCGGTCAAGGATATGCT 300
QY 489 cagcaacaagaagtcacctaatgttcaatcagatgcagatctatcttttgaagaacca 548
DB 301 CAGCAACAAGAAGTCCTTATGTTCAATGATGATGATGATGATGATGATGATGATGAT 360
QY 549 agaagttcttattcttgggtgacaatactatcttggggaagttgggaaaga 606
DB 361 AGAAGTCTTATCTTTGGGTGAGACATTAATATCTCTGGGGAAGTTGGGAAAAAGA 418

RESULT 14
BI267321 663 bp mRNA linear EST 18-JUL-2001

LOCUS NF105B10INJF1089 Insect herbivory Medicago truncatula cDNA clone
DEFINITION NF105B10IN 5', mRNA sequence.
ACCESSION BI267321
VERSION BI267321.1 GI:14872243

KEYWORDS EST.
SOURCE bareil medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE 1 (bases 1 to 663)

AUTHORS Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and Samel,G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
JOURNAL Unpublished (2000)

COMMENT

Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
Email: kthorh@comp.uark.edu
Insert length: 663 Std Error: 0.00
Plate: 105 Row: B Column: 10
Seq primer: TCACACGAGAAACGATGAC.
Location/Qualifiers

FEATURES
SOURCE

1. 663
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/db_xref="taxon:3880"
/clone="NF105B10IN"
/clone_lib="Insect herbivory"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap. Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
BASE COUNT 205 a 132 c 134 g 188 t 4 others
ORIGIN

Query Match 27.8%; Score 413.8; DB 10; Length 663;
Best Local Similarity 78.4%; Pred. No. 6.2e-97;
Matches 520; Conservative 0; Mismatches 136; Indels 7; Gaps 2;

QY 34 actaagacacagactcttcaatgattgctatgacaccttggctatgtaagctgct 93
DB 7 ACAACAGACATGAGAGTTTCATTAATTAACATCATATTTACTCTTCTTGAGCCGTACA 66
QY 94 atctctctcccaataatctcggaacaacatctcatatgaaatcgtaaatattactcccc 153
DB 67 ATCTCTCTCCCAATATCTTGGAAACAATATCTCAACCAATGTAATAATATTTTC----- 121
QY 154 aaaatcagaaccagttacatatacgcgtgtatatatttgatgctggtgacatggaagc 213
DB 122 -CAAAACAGAAACCTTAACCTGTAAGCTGTCGCTTTGATGCTGTGACACCGGTAGC 180
QY 214 agatccatgcttcaatatttgatcagaactatgacatccctccgctggaacgaact 273
DB 181 CGGTTCATCTTCACCATTTTGAATGATGAGAACTTGATCTTCTTACATTTGGCAACGATGTT 240
QY 274 gagtttattgattcgtttaaaccgggttgagttcattgaagcgttaacccgaagct 333
DB 241 GAGTTTATTAATAAGACAACACCCGGTTGAGGATACGAGATATATCAAAAGGAAGCA 300
QY 334 gcagaatcttgattccactcttaaaagaagcagaagaatggttccgttgagccagca 393
DB 301 GCAGAGTCTCTGATTCACATTTTGAAGCAAGAAAGATGCTTCTGTATCTGCAAA 360
QY 394 cccaacacccggttgaagcttggggaactgcagcaggttgaagcttttggagggaagtgct 453
DB 361 CCCAAACACCCGTTAAGCTTGGGCAACAGCCGGTTTAAAGGCTTTGATGGAATAATTTCT 420
QY 454 gctgaaatataattgcaagcgggtcaggatattgctcagaacaagaagtgccttaattgt 513
DB 421 TCCGAATTTGATTTGGAAGCGGTGTCGAGTTGCTCCTCAAAAAGAGAACGATTTAACGTA 480
QY 514 caatcagatgcagatctattcttggatggaaccagaaggttcttattcttgggtgagca 573

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